

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:25:49 ; Search time 21.01 Seconds

(without alignments)
3516.864 million cell updates/sec

Title: US-09-378-759-11

Perfect score: 5116

Sequence: 1 LLAAVEETLMDSTTATAEFG.....ILNSIQVRAQMNOIQSYEV 970

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5112	99.9	970	2 I78842	receptor protein-t
2	4950.5	96.8	995	2 A56599	embryo kinase 5 -
3	3914.5	76.5	984	2 A39753	protein-tyrosine k
4	3754	73.4	985	2 I51672	receptor tyrosine
5	3707	72.5	952	2 I50612	protein-tyrosine k
6	3649.5	71.3	988	2 I50611	protein-tyrosine k
7	3632.5	71.0	998	2 S37627	protein-tyrosine k
8	3604	70.4	993	2 I48653	mouse developmenta
9	3429	67.0	938	2 I49071	protein kinase - m
10	3060.5	59.8	985	2 I51549	receptor tyrosine
11	3031	59.2	986	2 I78844	receptor protein-t
12	3031	59.2	991	2 I78843	receptor protein-t
13	3026	59.1	986	2 S78059	protein-tyrosine k
14	3016	59.0	998	2 I58351	receptor protein-t
15	3001	58.7	998	2 JCS672	receptor tyrosine
16	2990	58.4	1013	2 I50615	receptor-tyrosine
17	2930	57.1	981	2 S51604	receptor-like tyro
18	2918.5	57.0	983	2 A38224	receptor-like tyro
19	2914	57.0	983	2 B45583	receptor tyrosine
20	2904	56.8	1005	2 S49015	receptor tyrosine
21	2875.5	56.2	983	2 A45583	receptor tyrosine
22	2835.5	55.4	987	2 I48652	mouse developmenta
23	2827.5	55.3	987	2 A54092	protein-tyrosine k
24	2792.5	54.6	987	2 I48953	eph-related recep
25	2714.5	53.1	849	2 I50617	protein-tyrosine k
26	2600	50.8	948	2 S51605	receptor-like tyro
27	2512	49.1	988	2 S47489	receptor tyrosine
28	2493	48.7	893	2 S51603	receptor-like tyro
29	2471	48.3	478	2 A57174	protein-tyrosine k

30	2466.5	48.2	480	2 I48760	protein-tyrosine k
31	2442	47.7	877	2 I48967	brain-specific kin
32	2438	47.7	1006	2 JCS526	kinase-defective E
33	2349.5	45.9	976	2 A36355	protein-tyrosine k
34	2340.5	45.7	977	2 S49004	tyrosine kinase Mp
35	2260.5	44.2	975	2 I48974	receptor protein t
36	2246	43.9	612	2 S33506	protein-tyrosine k
37	1923.5	37.6	1019	2 T13039	tyrosine kinase re
38	1856.5	36.3	984	1 A34076	protein-tyrosine k
39	1548	30.3	490	2 I50613	protein-tyrosine k
40	1477.5	28.9	605	2 JCS673	receptor tyrosine
41	1470	28.7	610	2 I48612	developmental kin
42	1467.5	28.7	626	2 I48614	developmental kin
43	1422	27.8	1122	2 T42400	Eph receptor tyros
44	1329	26.0	426	2 I48759	protein-tyrosine k
45	1252.5	24.5	919	2 T29581	hypothetical prote

ALIGNMENTS

RESULT 1
I78842
receptor protein-tyrosine kinase - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C:Accession: I78842
R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welch
Oncogene 10, 897-905, 1995
A:Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein
A:Reference number: I58351; MUID:95206782
A:Accession: I78842
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-970 <RES>
A:Cross-references: GB:I36643; NID:9551609; PIDN:AAA7424.1; PID:9551610
C:Genetics:
A:Gene: HEK5
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
F:603-871/Domain: protein kinase homology <Kin>
F:894-960/Domain: SAM homology <SAM>

Query Match	Score	5112	DB 2	Length	970
Best Local Similarity	99.9%				
Pred. No. 16-233					
Matches 969	Conservative	0	Mismatches 1	Indels	0
QY	1	LLAAVEETLMDSTTATAEFGMMVHPPSGMEVSGYDENMNTTITTYOVCHVFESSQNNMIR	60		
DB	1	LLAAVEETLMDSTTATAEFGMMVHPPSGMEVSGYDENMNTTITTYOVCHVFESSQNNMIR	60		
QY	61	TKTIRRGARHRIHVEKFFSVRDCSSIPVPGSCKEFFNYIYEADSDATKFPNNMEMP	120		
DB	61	TKTIRRGARHRIHVEKFFSVRDCSSIPVPGSCKEFFNYIYEADSDATKFPNNMEMP	120		
QY	121	WVKVDITIADESESOYDLGRVAKINTFVRSFGVRSFGYLAFOYGGCMSLIAVRVY	180		
DB	121	WVKVDITIADESESOYDLGRVAKINTFVRSFGVRSFGYLAFOYGGCMSLIAVRVY	180		
QY	121	WVKVDITIADESESOYDLGRVAKINTFVRSFGVRSFGYLAFOYGGCMSLIAVRVY	180		
DB	121	WVKVDITIADESESOYDLGRVAKINTFVRSFGVRSFGYLAFOYGGCMSLIAVRVY	180		
QY	181	RKCPRIIONGALFOETLSAESTSLVAAGSCIANAEVDVPIKLYCNDGEMLVPIGIC	240		
DB	181	RKCPRIIONGALFOETLSAESTSLVAAGSCIANAEVDVPIKLYCNDGEMLVPIGIC	240		
QY	241	MCKAGEAVENGTVCRGCGSGTFKANOGEACTHCPINSRTTSEGATNCVRNGYRADL	300		
DB	241	MCKAGEAVENGTVCRGCGSGTFKANOGEACTHCPINSRTTSEGATNCVRNGYRADL	300		
QY	301	DPIDMCTTIPAPQAVISSVNETSLMLETPPRDSGREDLVYNIKSCSGSGRACATR	360		
DB	301	DPIDMCTTIPAPQAVISSVNETSLMLETPPRDSGREDLVYNIKSCSGSGRACATR	360		
QY	361	CGDNVOYAROLGLTPRIYISDLAHOYTFEIAQVNVTOOSPPSPQFAVINTTQNA	420		
DB	361	CGDNVOYAROLGLTPRIYISDLAHOYTFEIAQVNVTOOSPPSPQFAVINTTQNA	420		

Db 361 CGDNVOAPRQLGLTEPRITISDLAHTQYTFEIQAVNGVTQSPSPQFASVNTTNOA 420
 QY 421 APSAIVIMHOVSRTVSTILSMQSDPQNGVILDYELQYERKLSYNTATKSPNTYT 480
 Db 421 APSAIVIMHOVSRTVSTILSMQSDPQNGVILDYELQYERKLSYNTATKSPNTYT 480
 QY 481 GLKAGAIYVQVARTVAGRYSGKMYFQTMTEAEYQTSIOEKPLIIIGSSAAGLVFLI 540
 Db 481 GLKAGAIYVQVARTVAGRYSGKMYFQTMTEAEYQTSIOEKPLIIIGSSAAGLVFLI 540
 QY 541 AVAVIAIVCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTYEDNEAVERAKET 600
 Db 541 AVAVIAIVCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTYEDNEAVERAKET 600
 QY 601 DISCVATIEOYIGAGEGECVSGHLKLPGRKEIFVALTKLSGTEKORRDFLSEASIMGO 660
 Db 601 DISCVATIEOYIGAGEGECVSGHLKLPGRKEIFVALTKLSGTEKORRDFLSEASIMGO 660
 QY 661 FDRPNVITHLEGVYTKSTPVMIITEFMENGLSDSFLRQNDQFQTVIOLVGMKRGIAAGMKY 720
 Db 661 FDRPNVITHLEGVYTKSTPVMIITEFMENGLSDSFLRQNDQFQTVIOLVGMKRGIAAGMKY 720
 QY 721 LADMNVVHRDLAARNILVNSNLVCKVSDGLSRFLSDPTTYSALGKFPITRTAPE 780
 Db 721 LADMNVVHRDLAARNILVNSNLVCKVSDGLSRFLSDPTTYSALGKFPITRTAPE 780
 QY 781 AIQYRKFTASDVWSYGIYVMEVNSYGERPYMDTODVYNAIEODYRLPPMDCCSALH 840
 Db 781 AIQYRKFTASDVWSYGIYVMEVNSYGERPYMDTODVYNAIEODYRLPPMDCCSALH 840
 QY 841 QLMIDCQKORNRHPRFGQIVNTLDKMRNPNSLKAMAPLSSGINPLDRTIPDYTSFN 900
 Db 841 QLMIDCQKORNRHPRFGQIVNTLDKMRNPNSLKAMAPLSSGINPLDRTIPDYTSFN 900
 QY 901 TYDEWLEAIKMGQYKESFANAGTSDVYSQMMEDILRQVTLAHOXKILNSIQVMA 960
 Db 901 TYDEWLEAIKMGQYKESFANAGTSDVYSQMMEDILRQVTLAHOXKILNSIQVMA 960
 QY 961 QMNOIOSVEV 970
 Db 961 QMNOIOSVEV 970
 RESULT 2
 A56599
 embryo kinase 5 - chicken
 N:Alternate names: receptor tyrosine kinase Cck5
 C:Species: Gallus gallus (chicken)
 C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 04-Feb-2000
 R:Pasquale, E.B.
 Cell:Regulatory 2, 523-534, 1991
 A:Title: Identification of chicken embryo kinase 5, a developmentally regulated receptor
 A:Reference number: A56599, M01D:92144672
 A:Accession: A56599
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-995 <PAS>
 A:Cross-references: GB:M62325; NID:q211448; PIDN:AAA48667.1; PID:q211449
 A:Note: sequence extracted from NCBI backbone (NCBIN:81999, NCBI:82001)
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein k
 F:628-896/Domain: protein kinase homology <KIN>
 F:636-644/Region: protein kinase ATP-binding motif
 F:919-985/Domain: SAM homology <SAM>

Query Match 96.8%; Score 4950.5; DB 2: Length 995;
 Best Local Similarity 95.6%; Pred. No. 4,2e-226;
 Matches 930; Conservative 28; Mismatches 12; Indels 3; Gaps 2;
 1 LLAAVEETLMDSTTATAELGMVHPSPSGMEVSGYDENMNTIRTYOVCAVFESSONMLR 60

Db 23 LLAAVEETLMDSTTATAELGMVHPSPSGMEVSGYDENMNTIRTYOVCAVFESSONMLR 82
 QY 61 TFFIRRGARHRIHVEKFSVRDCSSIPSPGCKEFENLYXEADEPDAKTFPMMEHP 120
 Db 83 TYIRRGARHRIHVEKFSVRDCSSIPSPGCKEFENLYXEADEPDAKTFPMMEHP 142
 QY 121 WVKVDITIADESEFQVLDLGRVAKINTEVRSFGPYSRSGFYLAPODYGCMSLIAVRFY 180
 Db 143 WVKVDITIADESEFQVLDLGRVAKINTEVRSFGPYSRSGFYLAPODYGCMSLIAVRFY 202
 QY 181 RRCPRITONGAIFQETFLCAESTSLVAANGSCIIANAEEVDVPIKLYCNGDGMLVPIGR 240
 Db 203 RRCPRITONGAIFQETFLCAESTSLVAANGSCIIANAEEVDVPIKLYCNGDGMLVPIGR 262
 QY 241 MCKAGEVAVENCTVCGCGSGTFKMGKANOGEACTHOPINSRTSEGAATNCVANGYRADL 300
 Db 263 MCKAGEVAVENCTVCGCGSGTFKMGKANOGEACTHOPINSRTSEGAATNCVANGYRADL 322
 QY 301 DPLDMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVNMLCKSCSGGRGACTR 360
 Db 323 DPLDMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVNMLCKSCSGGRGACTR 382
 QY 361 CGDNVOAPRQLGLTEPRITISDLAHTQYTFEIQAVNGVTQSPSPQFASVNTTNOA 420
 Db 383 CGDNVOAPRQLGLTEPRITISDLAHTQYTFEIQAVNGVTQSPSPQFASVNTTNOA 442
 QY 421 APSAIVIMHOVSRTVSTILSMQSDPQNGVILDYELQYERKLSYNTATKSPNTYT 480
 Db 443 APSAIVIMHOVSRTVSTILSMQSDPQNGVILDYELQYERKLSYNTATKSPNTYT 502
 QY 481 GLKAGAIYVQVARTVAGRYSGKMYFQTMTEAEYQTSIOEKPLIIIGSSAAGLVF 538
 Db 503 GLKAGAIYVQVARTVAGRYSGKMYFQTMTEAEYQTSIOEKPLIIIGSSAAGLVF 562
 QY 539 LIAVVIATVNC-RRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTYEDNEAVERA 597
 Db 563 LIAVVIATVNC-RRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTYEDNEAVERA 622
 QY 598 KEIDISCVATIEOYIGAGEGECVSGHLKLPGRKEIFVALTKLSGTEKORRDFLSEASI 657
 Db 623 KEIDISCVATIEOYIGAGEGECVSGHLKLPGRKEIFVALTKLSGTEKORRDFLSEASI 682
 QY 658 MGOFDHPRNVITHLEGVYTKSTPVMIITEFMENGLSDSFLRQNDQFQTVIOLVGMKRGIAAG 717
 Db 683 MGOFDHPRNVITHLEGVYTKSTPVMIITEFMENGLSDSFLRQNDQFQTVIOLVGMKRGIAAG 742
 QY 718 MKYLDAMNVVHRDLAARNILVNSNLVCKVSDGLSRFLSDPTTYSALGKFPITRTAPE 777
 Db 743 MKYLDAMNVVHRDLAARNILVNSNLVCKVSDGLSRFLSDPTTYSALGKFPITRTAPE 802
 QY 778 APEAIQYRKFTASDVWSYGIYVMEVNSYGERPYMDTODVYNAIEODYRLPPMDCCS 837
 Db 803 APEAIQYRKFTASDVWSYGIYVMEVNSYGERPYMDTODVYNAIEODYRLPPMDCCS 862
 QY 838 ALHQMLDQKORNRHPRFGQIVNTLDKMRNPNSLKAMAPLSSGINPLDRTIPDYT 897
 Db 863 ALHQMLDQKORNRHPRFGQIVNTLDKMRNPNSLKAMAPLSSGINPLDRTIPDYT 922
 QY 898 SFNTVDEWLEAIKMGQYKESFANAGTSDVYSQMMEDILRQVTLAHOXKILNSIQV 957
 Db 923 SFNTVDEWLEAIKMGQYKESFANAGTSDVYSQMMEDILRQVTLAHOXKILNSIQV 982
 QY 958 MRAQNOIOSVEV 970
 Db 983 MRAQNOIOSVEV 995
 RESULT 3
 A39753
 protein-tyrosine kinase (EC 2.7.1.112) elk precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 04-Feb-2000

Db 257 CKAGYEP-ENHVVCKACPAAMFKANOGMIGIACAPANSRSTSEASPICICRNGYTRADF 315
QY 302 PLDMPTTIPSAQAVISSVNETSIMELEWTPPRDSSGREDLVNITICKSCSGRGACTRC 361
Db 316 TPAPCTSPVSGRNVISIVNETAITLEMHPRETGTGRDGVNIVCKCRADRACSR 375
QY 362 GDNVQAPRGLTEPRITYSIDLTAHQYFEIQAANGVVDOSPFSOFASVITITNOAA 421
Db 376 DDNVVDVPRGLGLTRVFLISNMAHTPYFEIQAANGVYTNKSPFPQHVSVITITNOAA 435
QY 422 PSANVSMHOVSRTVDSITLWSQPDOPNGVILDELYQYKEKELSEYNAFAIKSPNTV-- 479
Db 436 PSSVPTMHOVKATMKISITLWSQPDOPNGIILDEYQYKEKELSEYNAFAIKSPNTV-- 495
QY 480 TGLKAAIYVE--OYRARVAGYGRYSGMRYQMTLEMYQTSIOEKLPLIIGSSAAGL 536
Db 496 TG--GRVMFMFSVQVRAKVAGYKGFSSQGRQTLAEYKSELREQLPL-NGSAAGV 551
QY 537 VFLIADVIAIVCNRRGFERADSEYTDKLOHYTSGHITFGMKIYIDPFIYEDPNEAVREF 596
Db 552 VFLIVSLAISIVCSRRKRTYSKEAVYSDKLOHYTSGRSPOMKIYIDPFIYEDPNEAVREF 611
QY 597 AKETIDISYKIEIOVIGAGEGVCYSGHLKPGKREIYFAIKTKISGYTERKORDFLSEAS 656
Db 612 AKETIDISYKIEIOVIGAGEGVCYSGHLKPGKREIYFAIKTKISGYTERKORDFLSEAS 671
QY 657 IMQOPHPVNIHEGYVSTPYMTTEPEMENGSLDSFLRONGQOTVYIOLVGMLEGIAA 716
Db 672 IMQOPHPVNIHEGYVSTPYMTTEPEMENGSLDSFLRONGQOTVYIOLVGMLEGIAA 731
QY 717 GMKYLADMYVHRDLAARNILVNSNLVCKVSDGSLRFLIEDTSDPTYSALGKPFPIRM 776
Db 732 GMKYLSEMYVHRDLAARNILVNSNLVCKVSDGSLRFLIEDTSDPTYSALGKPFPIRM 791
QY 777 TAPAEIQKRTSASDVMSYGIYVMEVMSYGERPYWMTNODVINAIEDYRLPPMDCP 836
Db 792 TAPAEIQKRTSASDVMSYGIYVMEVMSYGERPYWMTNODVINAIEDYRLPPMDCP 851
QY 837 SALHOLMLCOKDRNRHPRKFGQIVNTLDKMI RNPSLAKMAPLSSGIMLPLIDRTIPY 896
Db 852 SALHOLMLCOKDRNRHPRKFGQIVNTLDKMI RNPSLAKMAPLSSGIMLPLIDRTIPY 911
QY 897 TSEFTVDEMLEAIKMGQYKESFANAGTSEFDVYSQMMEDILRVGYTLAHOQKILNSIO 956
Db 912 TSEFTVDEMLEAIKMGQYKESFANAGTSEFDVYSQMMEDILRVGYTLAHOQKILNSIO 971
QY 957 VMRAQMNQ 964
Db 972 SMKVOITQ 979

RESULT 5
150612
protein-tyrosine kinase (EC 2.7.1.112) Cdk6 - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Feb-2000
C:Accession: I50612; S33503
R:Sajjadi, F.G.; Pasquale, E.B.
OncoGene 8, 1807-1813, 1993
A:Title: Five novelavian Eph-related tyrosine kinases are differentially expressed.
A:Reference number: 150611; MUID:93288394
A:Accession: I50612
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-952 <SA>
A:Cross-references: EMBL:Z19110; NID:G312901; PIDN:CAA79526.1; PID:G312902
C:Genetics: C6
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kinase
F:585-853/Domain: protein kinase homology <KIN>
F:593-601/Region: protein kinase ATP-binding motif
F:876-942/Domain: SAM homology <SAM>

Query Match 72.5%; Score 3707; DB 2; Length 952;
Best Local Similarity 70.2%; Pred. No. 1.5e-167;
Matches 687; Conservative 120; Mismatches 118; Indels 54; Gaps 4;
QY 7 ETLMDSTTATLGAIVGVHVPSSGMEVSYGDEMMNTIRYQVCNVPSSONNMILRTKPIRR 66
Db 1 ETLMDRTATLGAIVGVHVPSSGMEVSYGDEMMNTIRYQVCNVPSSONNMILRTKPIRR 60
QY 67 RGAHRIHVEKESVHDCSSIPSVGSKCTEFNLVYEADEFDSATKTFPMNMENPVKYDT 126
Db 61 RGAHRIHVEKESVHDCSSIPSVGSKCTEFNLVYEADEFDSATKTFPMNMENPVKYDT 120
QY 127 IAADEFSGYDLDGGRVMAKINTEVRSRFPVSRSGFYLAFOYGGCSLAVRFFRKCPPI 186
Db 121 IAADEFSGYDLDGGRVMAKINTEVRSRFPVSRSGFYLAFOYGGCSLAVRFFRKCPPI 148
QY 187 IONGALFOETLSGAEISTVAAARGSCIANAEYDVPYIKLYCNGDGBWLPYIGRCCKAGF 246
Db 149 VONFAIFPETMGANSTSLVYARGTIPNAEEYDVPYIKLYCNGDGBWLPYIGRCCKAGF 208
QY 247 EAVENGTVCRGCPSTCFKANOGEACTHCPINSRTSEGATNCVCNRYRADLPLDMP 306
Db 209 EP-ENNVACRACPACTEFKASQAGLCARCPNRSRSEASPLCACNGYFRADLPTPTA 267
QY 307 CTITPSAPAVISSVNETSIMELEWTPPRDSSGREDLVNITICKSCSGRGACTRCGDNVQ 366
Db 268 CTITPSAPAVISSVNETSIMELEWTPPRDSSGREDLVNITICKSCSGRGACTRCGDNVQ 327
QY 367 YAPRGLGLEPRITYSIDLTAHQYFEIQAANGVVDOSPFSOFASVITITNOAAPSAVS 426
Db 328 YAPRGLGLEPRITYSIDLTAHQYFEIQAANGVVDOSPFSOFASVITITNOAAPSAVS 387
QY 427 IMHOVSRTVDSITLWSQPDOPNGVILDELYQYKEKELSEYNAFAIKSPNTV-- 467
Db 388 IMHOVSRTVDSITLWSQPDOPNGVILDELYQYKEKELSEYNAFAIKSPNTV-- 447
QY 468 NATAIKSPNT--VIGLKGALIVYQVARYAGYGRYSGMRYQMTLEMYQTSIOEKL 525
Db 448 NATAIKSPNT--VIGLKGALIVYQVARYAGYGRYSGMRYQMTLEMYQTSIOEKL 507
QY 526 PLIGSSAAGVFIYSIVASIVCSRRKRAYSKYVYSDKLOHYTSGRSPOMKIYIDPFI 585
Db 508 PLIGSSAAGVFIYSIVASIVCSRRKRAYSKYVYSDKLOHYTSGRSPOMKIYIDPFI 567
QY 586 YEDPNEAVAREFAKEIDISCVKTEIOVIGAGEGVCYSGHLKPGKREIYFAIKTKISGYTE 645
Db 568 YEDPNEAVAREFAKEIDISCVKTEIOVIGAGEGVCYSGHLKPGKREIYFAIKTKISGYTE 627
QY 646 KORRDLSEASTMGQPDHPRNVTHLGVYTKSPVMTTEPEMENGSLDSFLRONGQOTVY 705
Db 628 KORRDLSEASTMGQPDHPRNVTHLGVYTKSPVMTTEPEMENGSLDSFLRONGQOTVY 687
QY 706 QLVGMILRGIAAGMYKYLADMYVHRDLAARNILVNSNLVCKVSDGSLRFLIEDTSDPTYT 765
Db 688 QLVGMILRGIAAGMYKYLADMYVHRDLAARNILVNSNLVCKVSDGSLRFLIEDTSDPTYT 747
QY 766 SALGKRPRTKMTAPARAIOYKRTSASDVMSYGIYVMEVMSYGERPYWMTNODVINAIED 825
Db 748 SALGKRPRTKMTAPARAIOYKRTSASDVMSYGIYVMEVMSYGERPYWMTNODVINAIED 807
QY 826 DYRLPPMDCPALHOLMLCOKDRNRHPRKFGQIVNTLDKMI RNPSLAKMAPLSSGIN 885
Db 808 DYRLPPMDCPALHOLMLCOKDRNRHPRKFGQIVNTLDKMI RNPSLAKMAPLSSGIN 867
QY 886 IPLDRTIPDYTSFNTVDEMLEAIKMGQYKESFANAGTSEFDVYSQMMEDILRVGYTLA 945
Db 868 IPLDRTIPDYTSFNTVDEMLEAIKMGQYKESFANAGTSEFDVYSQMMEDILRVGYTLA 927
QY 946 GHOKKIINSIOVMRAQMNQ 964
Db 928 GHOKKIINSIOVMRAQMNQ 946

RESULT 6

I50611

protein-tyrosine kinase (EC 2.7.1.112) Cdk10 - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text-change 04-Feb-2000

C:Accession: I50611; S33502

R:Sajadi, F.G.; Pasquale, E.B.

OncoGene 8, 1807-1813, 1993

A:Title: Five novel avian Eph-related tyrosine kinases are differentially expressed.

A:Reference number: I50611; MUID:93286394

A:Accession: I50611

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-988 <SAW>

A:Cross-references: EMBL:Z19061; NID:g312201; PIDN:CAW79511.1; PID:g312202

C:Genetics:

A:Gene: Cdk10

C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat

C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kinase

F:621-889/Domain: protein kinase homology <RNT>

F:629-637/Region: protein kinase ATP-binding motif

F:912-978/Domain: SAM homology <SAM>

[illegible]

Qy	655	ASIMQEPHPVNIHLEGVVKSTFPMITTEEMENGSIDSEFRONDGQFTVQLGMIRGI	714
Db	673	ASIMQEPHPNIHLEGVVKSRPMITTEEMENCALDSFLRLNDGQFTVQLGMIRGI	732
Qy	715	AAGMYTLADMTYVHRDLAARNILVNSNLVCKVSPFGLSRFIEDDTSPTYSALGGRFPI	774
Db	733	AAGMYTLESMNVHHDLAARNILVNSNLVCKVSPDGSLSRFIEDDPADPTYSLSLGGKIPi	792
Qy	775	RWTAPEAIOYKRFTSASDVWSYGIYVMEVMSYGERPYVDMTNODVINAIEODYRLPPMD	834
Db	793	RWTAPEAIALYKRFTSASDVWSYGIYVMEVMSYGERPYVDMNODVINAIEODYRLPPMD	852
Qy	835	CPSAIHOIMLQWCKDRHRKPFQOIVNTLQKMRNPSTLAKMPLSSGILPLDRTIP	894
Db	853	CPSTALHQLMLDQWADRRLRPFQOIVNTLQKLRINNAASLVIASVQSGVQPLDRTIP	912
Qy	895	DYTSENTVDEWLEAIKMQYKESFPANAGFTSFDDVSSOMMEDILRVGTVLGHOKKIILNS	954
Db	913	DYTTFTTQGDWIDAIKMKRYKENEFNAGFASFDVAOMTADLLRLIGTVLGHOKKIILNS	972
Qy	955	IQVMAONNOIQSEVY 970	
Db	973	IQDMRLQNMQTLPIVOY 988	

```

RESULT      7
S37627
protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human
C|Species: Homo sapiens (man)
C|Date: 19-May-1994 #sequence_revision 03-Aug-1995 #text_change 04-Feb-2000
C|Accession: S37627
R|Boehme, B.; Holtlich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Streibhardt, K.; Ru
Oncogene 8, 2857-2862, 1993
A|Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.
A|Reference number: S37627; MUID:93390963
A|Accession: S37627
A>Status: Preliminary
A|Molecule type: mRNA
A.Residues: 1-998 <BO>
A.Cross-references: EMBL:X75208; NID:q406867; PIDN:CMA53021.1; PID:q406868
C.Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repa
C.Keywords: ATP, phosphotransferase, transmembrane protein, tyrosine-specific protei
F.631.899/Domain: protein kinase homology <KIN>
F.639-647/Region: protein kinase ATP-binding motif
F.922-988/Domain: SAM homology <SAM>

Query Match          71.0%; Score 3632.5; DB 2; Length 998;
Best Local Similarity 70.5%; Pred. No.5.2e-164;
Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

QY    4 AVEETLMSTTAETAEIGMVAHPDPSGMEEVSGYDENMMNTIRTYOVNCVFESSONMKLRKF   63
      |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB    37 ALKETLMDTKVTSELATMTSHPESCGMEEVSGYDEAMNPDIRTYOVNCVFESSONMLRTGF   96

QY    64 IRRRAHRIHVEMKMSVDCCSIIPSPGCKTEFLXYLEEDFDSATKTFPMNMENPYVK   123
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB    97 IMRDVQRVRYELKFTVRDCNSIPNPGSKTEFLFYLEDSDVASSPFMENMPYVK   156

QY    124 VDTIADESFSGVDLAGGRMYKINTEVRSFGPYSRSGFIPLAFODYGCGASLIAYRFYRK   183
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB    157 VDTIAPDEFSLDAG---RVNTRYKRSFGPLSKAGFIPLAFODGACGLISVFAYKKC   212

QY    184 PRLIQNGALFOETLSGAESTSLVAARGSCIANAEEVDPIKLYCNGDDEMVLPIGRCKRC   243
      |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB    213 ASTTAGFALEPETLTGAETSLLVIAPGTICIPAIVAVSYPLKLYCNGDDEMMYPVAGCTCA   272

QY    244 AGFEAVENTCYVGPPSGPFKANGODEACTHCPIRSRTTSSECATCYCNRNGYRADLDPL   303
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB    273 TGEHRAAKSQCRPCRPSPYSKAKGEBGPCLPFRPSRITTSPTAASTCTCHNNPNRYADDSQA   332

QY    304 DMPCTTIPSAPDAVISVNETSLMLEMTPRPDGSGRDLVYNIICKSC--GSGRACTRC   361

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Db 333 DSACTTVPSPRGVSVNTSTLLEMSERDGLVRDLDLITVCKCKHAGASACSRG 392
QY 362 GDNVQAPAROLGLTEPRITYSDLAHTQYTFEIOAVNGVTDOSEFSPQASVNTTNOAA 421
Db 393 DDVVEFPRLGLSEPRVHTSHLAHRTYTFEIOAVNGVSGKSPLPRAVAANTTTNOAA 452
QY 422 PSAVSTIMHGVSRVDSSTTSMSPDQPNGVITLDELOYEKESEYNATIKSPNTV-- 479
Db 453 PSEVPILRLHSSGSSLTLSMAPERNGVILDEYEMKYFEK--SEGIASTVTSQMSVOL 510
QY 480 TGLKAGAIYFOYRARTVAGYGRGMYFQMTF-AEYQTSIOEKLPLITIGSSAIVF 538
Db 511 DGLRPARYVYVYRARTVAGYGRGMYFQMTF--SEGIASTVTSQMSVOL 570
QY 539 LIAVYVYIAYCNRRGERADSEYTDKLOHTYSGHITPGMKYIDPPTYEDPNAVEFAK 598
Db 571 VVAVVYIAYVCLRKORHSGDSEYTERKLOQY---IAPGKMYIDPPTYEDPNAVEFAK 626
QY 599 EIDISGVKIEOVITGAGEFEGVSGHILKLPGRKEIFVAIKTKSGYTEKORRDLSEASTM 658
Db 627 EIDVSCVKIEVITGAGEFEGVSGHILKLPGRKEIFVAIKTKSGYTEKORRDLSEASTM 686
QY 659 GQFDHNVITLHLEGVYTKSTPVMITTEFMENGSLDSEFLRNDQGFYIOLVGLRGIAAG 718
Db 687 GQFDHNVITLHLEGVYTKSTPVMITTEFMENGSLDSEFLRNDQGFYIOLVGLRGIAAG 746
QY 719 KYLADNNVYHRLAARNILVNSLVCKVSPFGLSRFLLEDTSPTTYSALGKFPRLMTA 778
Db 747 KYLSENNVYHRLAARNILVNSLVCKVSPFGLSRFLLEDTSPTTYSALGKFPRLMTA 806
QY 779 PEAIQYRKFTSADVWSYGIYVMEVWSYGERPYWMDTNOVINAIBODYRLPPMCPSPA 838
Db 807 PEAIARKFTSADVWSYGIYVMEVWSYGERPYWMDTNOVINAIBODYRLPPMCPSPA 866
QY 839 LHOQMLDCKQKRNHRPKRGQIVNTLDKMTIRNPNSIKAMAPLSSGINLPDLRTIPDYS 898
Db 867 LHOQMLDCKQKRNHRPKRGQIVNTLDKMTIRNPNSIKAMAPLSSGINLPDLRTIPDYS 926
QY 899 FNTVDEMLEIKMGYKESFANAGFTSPDVYSGMMEDILRVGVTLAGHOKKILNSIQM 958
Db 927 FNTVDEMLEIKMGYKESFANAGFTSPDVYSGMMEDILRVGVTLAGHOKKILNSIQM 986
QY 959 RAQMOQIOSEV 970
Db 987 RLQMOQIOSEV 998

RESULT 8
148653
mouse developmental kinase 5 (MDK5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I48653
R:Clousek, T.; Lerch, M.M.; Ulrich, A.
Oncogene 11, 2085-2095, 1995
A:Title: Cloning, characterization, and differential expression of MDK2 and MDK5, two nc
A:Reference number: I48652; MUID:96074837
A:Accession: I48653
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-993 <RES>
A:Cross-references: EMBL:249086; NID:q1089899; PIDN:CAA88910.1; PID:q1089900
C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat
C:Keywords: ATP; transmembrane protein
F:626-894/Domain: protein kinase homology <KIN>
F:634-642/Region: protein kinase ATP-binding motif
F:917-983/Domain: SAM homology <SAM>

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Query Match 70.4%; Score 3604; DB 2; Length 993;
 Best Local Similarity 70.1%; Pred. No. 11e-162;
 Matches 683; Conservative 111; Mismatches 163; Indels 18; Gaps 6;

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QY 4 AVEETIMDSTTATAEIGMAYHPSSGWEVSGVDENNTTRITVOYCNVESSONMLRIKF 63
Db 29 ALRETTIMDTRKWTSELAMTSHPESSGWEVSGYDEANNPITRYOVYCNVRESSONMLRTGF 88
QY 64 IRRGARIHIVEKKFVRCROSSIPVPGSCKEFENLYYEADPDSATKTFPMNEMPMWK 123
Db 89 IMREYQRYVELKFTVRDONSIPNIPGSCKEFENLYYEADPDSATKTFPMNEMPMWK 148
QY 124 VDTIADESEFOYDAGRYMKINTEVRSFPGVSRSGFYLAFOYGGCMILAVRYEYRK 183
Db 149 VDTIADESEFRDAG---RVNTKYRSFGLSKAGFYLAFOYGGCMILAVRYEYRK 204
QY 184 PRILONGAIFOEILSABESTSLVAANGSCILANAEVDVYIKLYCNGDGWLYPIGRMCK 243
Db 205 ASTTAGFALFPELTLNGAEPSTLVAIPGTCILANAEVSVPLKLYCNGDGWLYPIGRMCK 264
QY 244 AGFEAVENGTCVCGPSGFGFNKNOGDEACTHCPINRRTSEGTNCVCRNGYRADLPL 303
Db 265 TGEHRAKSSQCRACPGSYAKAKOGGCPPLPCPPNRTTSPAASICTCHNNFYRADSDSA 324
QY 304 DMECTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVNITCKSCSGSGA----C 358
Db 325 DSACTTEPSPRGVSVNNTSTLLEMSERDGLVRDLDLITVCKCKHAGASACSRG 384
QY 359 GQFDHNVQAPAROLGLTEPRITYSDLAHTQYTFEIOAVNGVTDOSEFSPQASVNTTNO 418
Db 385 SRCDVVEFPRLGLSEPRVHTSHLAHRTYTFEIOAVNGVSGKSPLPRAVAANTTTNO 444
QY 419 QAPASVSTIMHGVSRVDSSTTSMSPDQPNGVITLDELOYEKESEYNATIKSPNTV 478
Db 445 QAPASVPTLHLHSSGSSLTLSMAPERNGVILDEYEMKYFEK--SKIASTVTSQMSVOL 502
QY 479 V--TGLKAGAIYFOYRARTVAGYGRGMYFQMTF-AEYQTSIOEKLPLITIGSSAAG 535
Db 503 VQDGLDQPARVYVYRARTVAGYGRGMYFQMTF--SEGIASTVTSQMSVOL 562
QY 536 LVEFLAVVYIAYCNRRGERADSEYTDKLOHTYSGHITPGMKYIDPPTYEDPNAVEFAK 595
Db 563 FVFMVYVYIAYVCLRKORHSGDSEYTERKLOQY---IAPGKMYIDPPTYEDPNAVEFAK 618
QY 596 FAKEDISCVKIEOVITGAGEFEGVSGHILKLPGRKEIFVAIKTKSGYTEKORRDLSEASTM 655
Db 619 FAKEDVSCVKIEVITGAGEFEGVSGHILKLPGRKEIFVAIKTKSGYTEKORRDLSEASTM 678
QY 656 SINGQFDHNVITLHLEGVYTKSTPVMITTEFMENGSLDSEFLRNDQGFYIOLVGLRGIA 715
Db 679 SINGQFDHNVITLHLEGVYTKSTPVMITTEFMENGSLDSEFLRNDQGFYIOLVGLRGIA 738
QY 716 AGMKYIADNNVYHRLAARNILVNSLVCKVSPFGLSRFLLEDTSPTTYSALGKFPRLMTA 775
Db 739 AGMKYIADNNVYHRLAARNILVNSLVCKVSPFGLSRFLLEDTSPTTYSALGKFPRLMTA 798
QY 776 WTAPAIQYRKFTSADVWSYGIYVMEVWSYGERPYWMDTNOVINAIBODYRLPPMCPSPA 835
Db 799 WTAPAIARKFTSADVWSYGIYVMEVWSYGERPYWMDTNOVINAIBODYRLPPMCPSPA 858
QY 836 PALHQLMLDCKQKRNHRPKRGQIVNTLDKMTIRNPNSIKAMAPLSSGINLPDLRTIPD 895
Db 859 PALHQLMLDCKQKRNHRPKRGQIVNTLDKMTIRNPNSIKAMAPLSSGINLPDLRTIPD 918
QY 896 YTSFNTVDEMLEIKMGYKESFANAGFTSPDVYSGMMEDILRVGVTLAGHOKKILNSIQM 955
Db 919 YTSFNTVDEMLEIKMGYKESFANAGFTSPDVYSGMMEDILRVGVTLAGHOKKILNSIQM 978
QY 956 QVRAQMOQIOSEV 970
Db 979 QVRAQMOQIOSEV 993

RESULT 9
149071
protein kinase - mouse (fragment)

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```

Db 441 STVTQIQPKETIRHSYSLTWPEPERANGVITLVEVYKYEKKDQNERSYRIYKTKASRSADIK 500
OY 481 GLKAGAIYVQVARYVAGYGRISGKMYFQTMTEAEYQTSIOEKPLITISSAAGVELI 540
Db 501 GLMPLTGYFHVHAKRAAGAGFEFSGPEFTNTVPSPMIG-EGTSPVLLVYVAGSIVLV 559
OY 541 AAIVVIAIVCRR--GFERADSEYTDKLOHTSGHIFPGMKIYIDPFEPNPAVREFAK 598
Db 560 VIIIAAFVISRRSKSKAKQADEE-----KHLNOGVATYTDPTFYEDPPNAVREFAK 613
OY 599 EIDISCVKIEOVIVGAGFEFGVSGHLKPGKREIFAIAIKLKSQYTEKQRRDLSEASIM 658
Db 614 EIDASCIKIEKIVGVGEFGVSGRLKPGKREIYVAKITLKGAYTDKQRRDLSEASIM 673
OY 659 GQDPHNVHILEGVYTKSTPVMITTEFMENGSLDPSLRONDGQFTYQVLYGMRLGIAAG 718
Db 674 GQDPHNPRIHILEGVYTKCKPMITTEFMENGSLDAFLRKNDGRTYQVLYGMRLGIGSGM 733
OY 719 KYLADMYVHRDLAARILVNSMLVCKVSDPGLSRFLEDTSPTYSALGSKREPIRMTA 778
Db 734 KYLSDMSTYHRDLAARILVNSMLVCKVSDPGLSRFLEDTSPTYSALGSKREPIRMTA 791
OY 779 PEAIQYRKFTSASDVMSYGIWMEVMSYGERPYMDTNDQVINAIBODYRLPEPMDCPSA 838
Db 792 PEAIQYRKFTSASDVMSYGIWMEVMSYGERPYMDTNDQVINAIBODYRLPEPMDCPSA 851
OY 839 LHLQMLDMCKDKNNHRPKFGQIYVNTLDKMTIRNNSLKAAPLSSGINTPLDRTIPYTS 898
Db 852 LHLQMLDMCKDKNNHRPKFGQIYVNTLDKMTIRNNSLKAAPLSSGINTPLDRTIPYTS 911
OY 899 FNVVDEMLEIKKQYKESFANAGFTSFVYVSOMMEDILRVGVTLAGHOKILNSTIOM 958
Db 912 VASVLDWMLQSKRRKRDNTAGYTSLEAVYVAVNODDLTRIGISISHQNKILISVQGM 971
OY 959 RAQMNOIQ 966
Db 972 RTQLOQMO 979

```

RESULT 11

178844

receptor protein-tyrosine kinase - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000

C:Accession: I78844

R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995

A:Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein-ty A:Reference number: I58351; MUID:95206782

A:Accession: I78844

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-966 <RES>

A:Cross-references: GB:I36645; NID:9551613; PIDN:AAA74246.1; PID:9551614

A:Genetics:

A:Gene: HEK8

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat F:619-885/Domain: protein kinase homology <Kin>

F:908-974/Domain: SAM homology <SAM>

Query Match 59.2%; Score 3031; DB 2; Length 986;

Best Local Similarity 59.3%; Pred. No. 1.1e-135;

Matches 580; Conservative 142; Mismatches 214; Indels 42; Gaps 13;

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OY 4 AVEETLMDSTTATAELGMVHP-PSGMEVSYGDENNMTIRTYOVGVFESSONNMLRTK 62
Db 28 ANEVITLLDSVSGELGMVHP-PSGMEVSYGDENNMTIRTYOVGVFESSONNMLRTD 87
OY 63 FIRRGAHRIHVEKMFVSRDCSSIPVPSGCKTFNLVYVYVYVYVYVYVYVYVYVYV 122
Db 88 WITREGAQRVYIRIKFTLRDCNSLPGVMGCKETFNLYYESSNDKERFI---RENQFV 143

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OY 123 KVDITADESEFSQVNDIGGRVYKINTEVRSFPGYRSAGFYLAPODYGCGMSLAVRYFRK 182
Db 144 KIDITIADESEFTQVNDIGDRIMKINTEIRVDYVGLSKGFIYAFDVCACIALVSVRYFRK 203
OY 183 CPRIIONGALFQETLSGAESTSLVAARSGCIANAEEVDVPIKLYCNGDEWMLVPIRCMK 242
Db 204 CPLTVRLAQFPPTITGADTSLVLEYRSGCVNNSSEKDV-KMYCGADGEMVLVPIGNCJC 262
OY 243 KAFPEAVENGSTVCRGCPSPGIFKANQDDEACTHCPINSRITTSSEATATVCVCRNGYRADD 302
Db 263 NACHE--ERSGEQVAKIGYKALSTDATCAKCPHPSYVWEATATCTDGRFFRADNDA 320
OY 303 LDMPCRTIPAPQAVIASSVNETSLMEWPPRDSGGEDIVYNIICKSGSG-RGACTRC 361
Db 321 ASMPCTRPSPAPLNLISNNETSYNLEWSSPONTGGRQDITVYVCKKCGAGPSCRC 380
OY 362 GDNVQYAPROGLTFEPRIYISDLAHTQYTFELQAVNGVTDQSPSPQASVNTINQA 421
Db 381 GSGVHTPQONGKLTQKVSITDLAHTNYFEIWAANGSVKYNPNPDQSVYVTTNQAA 440
OY 422 PSAVSTMHQVSRVYDITSLWSQPDQPNVYILDYEQYKEKSE--YNAATKSTNTY 479
Db 441 PSSIALVQAKEVTRYVALAMLEPDRNGVILEYEVYKYEKKDQNERSYRIYKTKASRSADIK 500
OY 480 TGLKAGAIYVQVARYVAGYGRISGKMYFQTMTEAEYQTSIOEKPLITISSAAGVELI 540
Db 501 GLMPLTGYFHVHAKRAAGAGFEFSGPEFTNTVPSPMIG-EGTSPVLLVYVAGSIVLV 559
OY 532 --SAGLVFLIAVVAIVACNR--GFERADSEYTDKLOHTSGHIFPGMKIYIDPFEPNPAVREFAK 598
Db 550 LVSQSVYVLLVIAAFVISRRSKSKAKQADEE-----KHLNOGVATYTDPTFYEDPPNAVREFAK 613
OY 588 DNEAVREFAKETDSCVRIEQYVIGAGEFGVSGHLKPGKREIFAIAIKLKSQYTEKQRRDLSEASIM 647
Db 604 DNEAVREFAKETDSCVRIEQYVIGAGEFGVSGHLKPGKREIFAIAIKLKSQYTEKQRRDLSEASIM 663
OY 648 RQDFTSEASIMQFQDPHNPVHILEGVYTKSTPVMITTEFMENGSLDPSLRONDGQFTYQVLYGMRLGIAAG 718
Db 664 RQDFTSEASIMQFQDPHNPVHILEGVYTKSTPVMITTEFMENGSLDPSLRONDGQFTYQVLYGMRLGIAAG 723
OY 708 VGMRLGIAAGMKTADMTVYHRDLAARILVNSMLVCKVSDPGLSRFLEDTSPTYSALGSKREPIRMTA 778
Db 724 VGMRLGIAAGMKTADMTVYHRDLAARILVNSMLVCKVSDPGLSRFLEDTSPTYSALGSKREPIRMTA 791
OY 768 LGKFPTRMTPAPRAIYQYRKFTSASDVMSYGIWMEVMSYGERPYMDTNDQVINAIBODYRLPEPMDCPSA 838
Db 783 LGKFPTRMTPAPRAIYQYRKFTSASDVMSYGIWMEVMSYGERPYMDTNDQVINAIBODYRLPEPMDCPSA 851
OY 828 RLPPMDCPALHQLMDCMKDKNNHRPKFGQIYVNTLDKMTIRNNSLKAAPLSSGINTPLDRTIPYTS 898
Db 842 RLPPMDCPALHQLMDCMKDKNNHRPKFGQIYVNTLDKMTIRNNSLKAAPLSSGINTPLDRTIPYTS 911
OY 888 LDRTPDYTSFNTVDEMLEIKKQYKESFANAGFTSFVYVSOMMEDILRVGVTLAGH 947
Db 902 LDRTPDYTSFNTVDEMLEIKKQYKESFANAGFTSFVYVSOMMEDILRVGVTLAGH 961
OY 948 QKILINSIQVMARQNOI 965
Db 962 QKILINSIQVMARQNOI 979

```

RESULT 12

178843

receptor protein-tyrosine kinase - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999

C:Accession: I78843

R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995

A:Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein A:Reference number: I58351; MUID:95206782

A:Accession: I78843

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-991 <RES>
 A:Cross-references: GB:L36644; NID:g551611; PIDN:AAA74245.1; PID:g551612
 C:Genetics: HEK7
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 F:627-893/Domain: protein kinase homology <kin>
 F:916-982/Domain: SAM homology <SAM>

Query Match 59.2%; Score 3031; DB 2; Length 991;
 Best Local Similarity 59.1%; Pred. No. 1,9e-135;
 Matches 567; Conservative 163; Mismatches 216; Indels 14; Gaps 10;

QY 6 EETLMDSTTATAEELGMVHPPSGMEVSGYDENNTIRTYQVCNVPFSSONNMLRTKFR 65
 DB EVNLDSRTVWGDLGMIAPKNGMEIEGVDENAPRHTYQVCNVMQNNMLTSMIS 95
 QY 66 RRGARHRIHVEKREVSRRCCSSIPSPGSKETFNLYYEADPDSATKTFPMNMPWYKVD 125
 DB 96 NEGSRRIEIEIKFTLRCCNSLPGLGTCCKETFMNMYFESDQNGR---NIKEQYIKID 151
 QY 126 TIADESFQVDLGRVYMKINTFVRSRSGFYAFQDYGCGMSLAVRVEYRRCPR 185
 DB 152 TIADESFTELDGRVYMKINTFVRSRSGFYAFQDYGCGMSLAVRVEYRRCPR 211
 QY 186 TIONGAIFQETLSGAEVSTLVAAKSGCIANAEEVDVPIKLYCNGDEMLVPIGRCKAG 245
 DB 212 VVRLHAFVPTITIGADSSQLLEVSQSCV-NH5VYDEPRPKMHCSEGLMVLPIGCKMCKAG 270
 QY 246 FEAVENTVRCRGSSTFRKANQGDCACTHCPINSRTTSEGATNCVCKNGYRADLDPLDM 305
 DB 271 YEE-KNKT-QOVCPKPGFKASPHLQSGCKPPEHYTHEASTVSCCKDPFRRESDDPTM 328
 QY 306 PCETTPAPDAVISVNETSLMELMTPPRDGGREDLVYNIICKSGSGGACTRCGDV 365
 DB 329 ACRTPRPAPRNALSNVETSEVLEMPRPADTGKRDVSYIACKCKSHAGVCECGGHV 388
 QY 366 QYARQGLTEPRITYSIDLAAHTQYTFEIOAVNGVTQDSPSPFOPASVNTTNOAPSAY 425
 DB 389 RYLPKROGLKNTSVMYMDLLAHTNYTFEIAVNGVSDLSGARGVSVNTTNOAPSAY 448
 QY 426 SIMHOVSRTVDSITLSMSQDOPRGVILDELOYEKELESEYNATKSPNTYT--GLK 483
 DB 449 TNNKKGIAKNSISLSQEDRPGIILEYKIKHEKD-OETSYTIKSKETTYTAGLK 507
 QY 484 AGAIYVQVARTVAGYGRYSCKMYFQMTAEAYOTSIQKELPLIGSSAAGFLAVV 543
 DB 508 PASVYVQIARTAGCYVSRREFET-TPVFAASDQGIPIYAVSVYGVILLAVI 566
 QY 544 VIAIVCNRGFERADSEYTDKIQHTYSGHI-TPGMKIYIDPFTYEDPNEAVREFAKEDI 602
 DB 567 GVLISGRRCYSKAKODPEEKMHFNHGHILKPGVRYIDPHYTEPNOAVHEPAKIEA 626
 QY 603 SCVKIEOVITAGEGEVCSHLKLPGRKELFVVAIKTLKSYTERQORDFSEASIMQED 662
 DB 627 SCITIEVITAGEGEVCSHLKLPGRKELFVVAIKTLKSYTERQORDFSEASIMQED 666
 QY 663 HPNVILLEGVYVTKSTPYMITTEFMENGLSDSFLRONDQFTYIQLVGLGIAAGMYLA 722
 DB 687 HPNIIHLEGVYVTKSTPYMITTEFMENGLSDSFLRONDQFTYIQLVGLGIAAGMYLA 746
 QY 723 DMNVYHDLAARILNLSNLCVAVSDFGLSRLEDDTSDFTYVSAIGKFPFIMWAPAEAL 782
 DB 747 DMNVYHDLAARILNLSNLCVAVSDFGLSRLEDDTSDFTYVSAIGKFPFIMWAPAEAL 804
 QY 783 QYKRTFSASQVMSYGIYVMEVSGERYMDMTNOVYINAEEDYRLPRMDCPSALHOL 842
 DB 805 AFKRTFSASQVMSYGIYVMEVSGERYMDMTNOVYINAEEDYRLPRMDCPSALHOL 864
 QY 843 MLDCCOKDRNHRKFGQIVNTLDKMIKRNPSLKAMAPLSSGINLPLDRTIPDYTSNTV 902
 DB 865 MLDCCOKDRNHRKFGQIVNTLDKMIKRNPSLKAMAPLSSGINLPLDRTIPDYTSNTV 924

QY 903 DEWLEAIKMGQYKESFANAGTFSEVYSQMMEDILRVGVTLAGHOKRIINSIQVNRQM 962
 DB 925 GEMLEAIKMGRTYEIFEMENGYSSMDVAQVTLIEDLRGLVGLVGHOKKINSIQEMKVL 984

RESULT 13

protein-tyrosine kinase (EC 2.7.1.112) Eph precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 19-Nov-1997 #sequence, revision 05-Dec-1997 #text, change 04-Feb-2000

C:Accession: S78059; S30505; I58366

R:Charney, P.
 submitted to the EMBL Data Library, March 1992

A:Reference number: S78059

A:Accession: S78059

A:Molecule type: mRNA

A:Residues: 1-986 <CHA>

A:Cross-references: EMBL:X65138; NID:g54083; PIDN:CAA46268.1; PID:g54084

R:Gillard-Hennessy, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chester, A.; Wilkin
 Oncogene 7, 2499-2506, 1992

A:Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed 1

A:Reference number: S30496; MUID:93096404

A:Accession: S30505

A:Molecule type: mRNA

A:Residues: 1-31,55-986 <GIL>

A:Cross-references: EMBL:X65138

C:Genetics: Sek

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase

F:1-15/Domain: signal sequence #status predicted <Sig>

F:16-986/Product: protein-tyrosine kinase Eph #status predicted <NMT>

F:548-569/Domain: transmembrane #status predicted <TM>

F:619-885/Domain: protein kinase homology <kin>

F:627-635/Region: protein kinase ATP-binding motif

F:908-974/Domain: SAM homology <SAM>

F:235,340,408,423/Binding site: carboxyrate (Asn) (covalent) #status predicted

Query Match 59.1%; Score 3026; DB 2; Length 986;
 Best Local Similarity 59.3%; Pred. No. 1,9e-135;
 Matches 580; Conservative 144; Mismatches 212; Indels 42; Gaps 14;

QY 4 AVEETLMDSTTATAEELGMVHPPSGMEVSGYDENNTIRTYQVCNVPFSSONNMLRTKFR 62
 DB 28 ANEVTLDSVSGVGLGMIAPKNGMEIEGVDENAPRHTYQVCNVMQNNMLTSMIS 87
 QY 63 FRRGARRHRIHVEKREVSRRCCSSIPSPGSKETFNLYYEADPDSATKTFPMNMPWYKVD 122
 DB 88 WITREGAORVYIEIKFTLRCCNSLPGLGTCCKETFMNMYFESDQNGR---NIKEQYIKID 153
 QY 123 KVTIADSEFSQVDLGRVYMKINTFVRSRSGFYAFQDYGCGMSLAVRVEYRRCPR 182
 DB 144 KVTIADSEFSQVDLGRVYMKINTFVRSRSGFYAFQDYGCGMSLAVRVEYRRCPR 211
 QY 183 TIONGAIFQETLSGAEVSTLVAAKSGCIANAEEVDVPIKLYCNGDEMLVPIGRCKAG 242
 DB 204 CPTLVNRLAQFPTITIGADSSQLLEVSQSCV-NH5VYDEPRPKMHCSEGLMVLPIGCKMCKAG 270
 QY 243 KAFEAVENTVRCRGSSTFRKANQGDCACTHCPINSRTTSEGATNCVCKNGYRADLDPLDM 302
 DB 263 KAFEAVENTVRCRGSSTFRKANQGDCACTHCPINSRTTSEGATNCVCKNGYRADLDPLDM 328
 QY 303 LBPCTTPAPDAVISVNETSLMELMTPPRDGGREDLVYNIICKSGSGGACTRCGDV 361
 DB 321 LBPCTTPAPDAVISVNETSLMELMTPPRDGGREDLVYNIICKSGSGGACTRCGDV 388
 QY 362 GDNVYARQGLTEPRITYSIDLAAHTQYTFEIOAVNGVTQDSPSPFOPASVNTTNOAPSAY 421
 DB 381 GDNVYARQGLTEPRITYSIDLAAHTQYTFEIOAVNGVTQDSPSPFOPASVNTTNOAPSAY 440
 QY 422 PSANVSIHVOVSRTVDSITLSMSQDOPRGVILDELOYEKELESEYNATKSPNTYT--GLK 483

[illegible]

Query Match 59.0%; Score 3016; DB 2; Length 998;
Best Local Similarity 59.1%; Pred. No. 5.7e-135;
Matches 574; Conservative 151; Mismatches 224; Indels 22; Gaps 10

[illegible]

Db	89	WISGNAQRIPELVEKATLRLRCNSLPVGLGCKETFMUYIYEDYD---TGNINENLYV	144
Qy	123	KVDYIADDESFOYDGLGRVMKINTEVERSFVYSRSGFYLAFOYGGCNSLIARVEYRK	182
Db	145	KIDYIADDESPQDGLGERMKINTEVERIGLPSKRGFYLAFOYACIALYASVYRYKK	204
Qy	183	CPRIYONCAIFOEFLSQAESTSYAARGSTIANA-EVDYVPIKLYONGBGEMLYVIGCM	241
Db	205	CWSTINELIATPEIDTVISEFSLSLVERGTCVSSAEAEANAPRMHCOSAGEVLYIGCTI	264
Qy	242	CKAGFEAEVNGTVCJRQPSGTFRKANOGDEACTCPIINSTRTESEGATNCGRNYYRADLD	301
Db	265	CKAGYQ-QKGDICEQSGRGFRFYKSSSQDQCSNCPIHFSDSKEGSSRCBEDGYRABSD	322
Qy	302	PLDMPCITTSAPQAVISSYNETSLIMEWTPPDSCGREDLYVNIITCKSCSGRACIIRC	361
Db	323	PPYVACTRPPSAPONLJFNINQTTVSLSEMSPPADNGBRDYVIRILCKCSWEQECVPC	382
Qy	362	GDNQVYAPBROGLGEEPRYIYSIDLLAHQYFFELQVQANQDQSPSPQASVNIITNOAA	421
Db	383	GSNIGYAPQDQGLDEDNYVMDLHAHANTYFEVEAYNGSDLSRSRQLRFLAASITTGAA	442
Qy	422	PSAYSIMHOVSRTVDJITLSMSQPDQPNVILYDELOYEKEELSE--YNAATIKSPNTV	479
Db	443	PSQYSGVAKREVLQRSYELSEMOEPHEHNGVITEYKEIYEKDOREKTYSTVTKTASAI	502
Qy	480	TGLKAGAIYVQVAKRVAVQYGRYSGKMYQVMTFA----EYQNSIQKLDPLIIGS--S	532
Db	503	NMLRPGYVYVQIAKFTAAAGISGNSPLDVALTEEAATGKMFETAYVSSQBNPVIIIAVYA	562
Qy	533	AAGLVFLIAVVVIAIVCNRR-GEFRADESETDKLOHYTSGHITPGMKITIDPTEYENE	591
Db	563	VAGTIIIVPMVFGTIIQRRIHCGYSKADQEBEDLYHFH--FPQYKTYIDPETYEDPNR	619
Qy	592	AVREFAKEIDISCVKLEQVIGAGBFEVCSGHLKLPGRKEIYVAIKTLKSGTTEQORDF	651
Db	620	AVHOFAKELDASCIRIERYVIGAGFEFGVCSGRKLKGRDVAVALIKTLGVGTQORDF	679
Qy	652	LSBASIMQOPHPVNIHLBEVYTKSPRVYMIITEPFMNGSIDSLFRLRONDQOPVYIOYGL	711
Db	680	LCBASIMQOPHPVNIHLBEVYTKGRKPVYMIITEFMENGALDAFLRKHDQOPVYIOYGL	739
Qy	712	RGIAAGMKYIADNMYVHRDILAAARNILVNSNLVCVSDFGLSRFLBEDDTSPTYTSALGK	771
Db	740	RGIAAGMKYIADMGVYHRDLAARNILVNSNLVCVSDFGLSRIYEDD-DEAVYTTT-GSK	797
Qy	772	FPRIKTADEALIQYKFTPSASDWSYGTIVMEVWNSYGERPYMDKTONDYVINALBEDYRLP	831
Db	798	IPVRYTADEALIQYKFTPSASDWSYGTIVMEVWNSYGERPYMDMSNDQVILKALEBGRIPA	857
Qy	832	PMDCSALHOMLMLCQKDRNHRPKFOIYVNTLDKMIIRNPNSILKAAPLSSGINPLDR	891
Db	858	PMDCPAGIHOMLMLCQKREAREKRFQIYIGIILDKMIIRNPNSILKTPGLGCSNPISPLDO	917
Qy	892	TIPDYTSENTVDEWLEAKIMQGYKESFANAGTSPDVNSQOMMEDILRYGVITLAGHOKKI	951
Db	918	NTPDPTTCSGVEMYLAIKIMERYKDNFTAGYNSLSEVARMETIEDVWNSIGITLVGHOKKI	977
Qy	952	LNSTQVMAQOM 962	
Db	978	MSSTQVMAQOM 988	

RESULT 15
jc5672
receptor tyrosine kinase (EC 2.7.-.-) Etk precursor - mouse
N|Alternates names: developmental_kinase_1
C|Species: Mus musculus (house mouse)
C|Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 18-Jun-1998
C|Accession: J05672, I4611, S51740
R|Talukder, A.H.; Muramatsu, T.; Kanada, N.
Cell Struct. Funct. 22, 477-485, 1997.

A:Title: A novel truncated variant form of Edb/MDKI receptor tyrosine kinase is expressed
 A:Reference number: JCS672; MUID:98035156
 A:Accession: JCS672
 A:Molecule type: mRNA
 A:Residues: 1-998 <TAL>
 A:Experimental source: embryo
 R:Clousek, T.; Millaer, B.; Ullrich, A.
 Oncogene 9, 97-108, 1995
 A:Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a novel
 A:Reference number: 148611
 A:Accession: 148611
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-998 <RES>
 A:Cross-references: EMBL:X79082; NID:6607133; PIDN:CA55687.1; PID:6607134
 C:Comment: This enzyme plays a role during development involving differentiation and pnc
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
 C:Keywords: ATP; brain; phosphotransferase; transmembrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-998/Product: receptor tyrosine kinase Edb #status predicted <MNT>
 F:31-553/Domain: extracellular #status predicted <EXT>
 F:331-438/Domain: fibronectin type III repeat <FN1>
 F:441-534/Domain: fibronectin type III repeat <FN2>
 F:554-579/Domain: transmembrane #status predicted <TM>
 F:631-897/Domain: protein kinase homology <KIN>
 F:639-647/Region: protein kinase ATP-binding motif
 F:920-986/Domain: SAM homology <SAM>

Query Match 58.7%; Score 3001; DB 2; Length 998;
 Best Local Similarity 58.6%; Pred. No. 2.9e-134;
 Matches 572; Conservative 155; Mismatches 217; Indels 32; Gaps 12;

3 AAVETLNDSTTAAELGMAVPPSGMEVSGYDENMNTITTYOVANVFESSQNNMLRTK 62
 29 AAKEVLLDSDAAGTELEWISSPPSGMEISGLDENYTPRTYOVCOVMEPNQNNMLRTN 88
 63 FIRRGARHRIHVEKFSVRDSSIPVSGCKETFNLYYVADFDSDATKTFPPNMENPMV 122
 89 WISKGNAGRIVELKFTLRDQNSLPGLVGTCKETFNLYYVADFDSDATKTFPPNMENPMV 144
 123 KVDITLADDESQVLDGGRWVKINTEVRSFGVRSRSGFYLAFOYGGCMSLIAVRFYRK 182
 145 KIDITLADDESFTQDLGERKKAKLTVREIGPLSKKGFYLAFOVACIALVSVKYYKK 204
 183 CPRIIONGAIFQETLSGAESTSLVAARGSCIAN-EEVDPIKIKYCNDSGEMLVPIGRCM 241
 205 CWTIVENLAVRPDTVSGSESLVEVNGTCVSSAEEDENSPRMHCESAEGEWLPIGKCI 264
 242 CKAGEFAVENGTVCRCGPGCTFRKNOGDEACTHCPINSRTTSEGATNCVCRNGYRADLD 301
 265 CKAGYQ--QKGDCEPCGRFRFYKSSQDLQSCNCPHSPFSDREGSSRCEDCGTYRAPSD 322
 302 PLDMRCTTIPSAPOAVSSVNETSLMLEWTPPRDSCGREDLVYNIITCKSGSGRGACTRC 361
 323 PPVYACTRPPSPAPONLLEFNINQTTVSLWSPADNGRNDVYRIILCKRCSEQGECPVC 382
 362 GDNVQVAPRQLGLEPRITISDLAHTQYTFEIOAVNGVTDOSPFSPOFASVNIITNOAA 421
 383 GSNIGVMPQOTGLEEDNVYMDLLAHANTFEVBAVNGVSDLSRSORLRAAVSITGQAA 442
 422 PSANVIMHOVSRIVDSITLSWSDOPDNGVILDELYEYKELSE--YNATAIKSPNTV 479
 443 PSQVSGVAKERVLQRSVOLSMOEPENGVITEYEIKYEEKDQREKRYSTLTKTSASASI 502
 480 TGLKAGAIYFOVARTVAGYGRSGKMYFQMTTEA-----EYQTSIOEKPLIIGS--S 532
 503 NNLKPGTVYVFOIRAVTAAGYGNKSPRLDVATLEASGKMEFATVAVSSQNPVITIAVVA 562
 533 AAGLVFLIAVVAIVAIQNR-GERADSEYTKLQHYTSGHITPGMKIYIDPFTYEDPNE 591
 563 VAGTIIILVWVFGFIIGRRHCGSKADQEDDELYFHK---FPCKTYIIDPFTYEDPNE 619

592 AVREPAKIDISCVKIEVYIGAGEFGEVCSGHLKLPCKREIYVAIKTKLKGYTEKORDF 651
 620 AVHQAPELNDSCIKIERVIGAGEFGEVCSGRLKLPORQVAVAIKTKLKGYTEKORDF 679
 652 LSEASINGOEPHNPVHLEGVVTKSTPVMITTEFENGSLDSFLRONDGQFTYQVGM 711
 680 LCEASINGOEPHNPVHLEGVVTKSTPVMITTEFENGSLDSFLRONDGQFTYQVGM 739
 712 RGIAGMKYLAADNMYVHRDLAARNILVNSMLVCVSDPGLSRELEDTSDPTYSALGK 771
 740 RGIAGMKYLAADNMYVHRDLAARNILVNSMLVCVSDPGLSRELEDTSDPTYSALGK 797
 772 FPIRMTAPEALQYKFTSASDWSYGVMEVMSYGERPYMDTNDQVYNAIEDYRLRP 831
 798 IPVMTAPEALQYKFTSASDWSYGVMEVMSYGERPYMDTNDQVYNAIEDYRLRP 857
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 887 PLDRITPDYTSFNTVDMELEAIKMGQYKESFANAGFTSFVYSQMMEDILRVGYTLG 946
 913 PLDQSTPDTAFCSVGEWLAIKMERYKDNFTYAGYNSLESVARMITIDVMSIGITLVG 972
 947 HOKKILNSIOVMAOM 962
 973 HOKKIMSSIOVMAOM 988

Search completed: July 24, 2001, 16:29:36
 Job time: 227 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:30:39 ; Search time 16.22 Seconds

(without alignments)
1204.704 Million cell updates/sec

Title: US-09-378-759-11

Perfect score: 970
Sequence: 1 LLAVEETLMDSTTATAEIG.....ILNSIQVRAQMOIQSVSEV 970

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 193259 seqs, 20144635 residues

Word size : 0

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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- 2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
- 4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
- 5: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
- 6: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	970	100.0	970	2	US-08-449-645A-11
2	970	100.0	970	2	US-08-702-367A-11
3	970	100.0	970	5	PCT-US95-04681-11
4	322	33.2	994	4	US-08-542-635-2
5	103	10.6	995	1	US-08-162-809-18
6	103	10.6	995	2	US-08-673-789-5
7	103	10.6	1011	1	US-08-162-809-12
8	40	4.1	998	2	US-08-449-645A-17
9	40	4.1	998	2	US-08-702-367A-17
10	40	4.1	998	5	PCT-US95-04681-17
11	40	4.1	998	5	PCT-US95-04681-2
12	39	4.0	59	1	US-08-222-616-25
13	39	4.0	59	2	PCT-US95-04228-25
14	37	3.8	57	2	US-08-456-647B-10
15	37	3.8	57	2	US-08-237-789A-10
16	36	3.7	612	2	US-08-673-789A-11
17	36	3.7	973	1	US-08-162-809-8
18	35	3.6	970	2	US-08-673-789-7
19	35	3.6	973	1	US-08-162-809-10
20	35	3.6	988	1	US-08-162-809-14
21	35	3.6	993	1	US-08-348-143-1
22	35	3.6	993	1	US-08-571-785-1
23	35	3.6	998	2	US-08-449-645A-20
24	35	3.6	998	2	US-08-702-367A-20
25	35	3.6	998	5	PCT-US95-04681-20
26	32	3.3	951	1	US-08-162-809-2
27	31	3.2	687	2	US-08-449-645A-29

28	31	3.2	687	2	US-08-702-367A-29	Sequence 29, Appl
29	31	3.2	849	1	US-08-162-809-6	Sequence 10, Appl
30	31	3.2	849	2	US-08-673-789-10	Sequence 6, Appl
31	31	3.2	984	2	US-08-673-789-6	Sequence 3, Appl
32	31	3.2	986	2	US-08-673-789-3	Sequence 15, Appl
33	31	3.2	986	2	US-08-449-645A-15	Sequence 15, Appl
34	31	3.2	986	2	US-08-702-367A-15	Sequence 15, Appl
35	31	3.2	986	5	PCT-US95-04681-15	Sequence 15, Appl
36	31	3.2	987	1	US-08-436-044-6	Sequence 6, Appl
37	31	3.2	987	2	US-08-436-044-6	Sequence 6, Appl
38	31	3.2	987	5	PCT-US95-08812-6	Sequence 36, Appl
39	31	3.2	1104	1	US-08-222-616-36	Sequence 36, Appl
40	31	3.2	1104	5	PCT-US95-04228-36	Sequence 36, Appl
41	31	3.2	1276	1	US-08-222-616-24	Sequence 24, Appl
42	31	3.2	1276	5	PCT-US95-04228-24	Sequence 24, Appl
43	30	3.1	976	2	US-08-449-645A-18	Sequence 18, Appl
44	30	3.1	976	2	US-08-702-367A-18	Sequence 18, Appl
45	30	3.1	976	5	PCT-US95-04681-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-449-645A-11
Sequence 11, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESS: Amgen Patent Operations/RBW
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-11

Query Match 100.0%; Score 970; DB 2; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAVEETLMDSTTATAEIGAMVHPSPGMEVSGYDENMTITRYOVANFESSONMLR 60
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QY 61 TKFIRRGARHIVHEKFSYVDCSSIPVSGCKETFNLYEADPDSATKTPNNMNEP 120
DB 61 TKFIRRGARHIVHEKFSYVDCSSIPVSGCKETFNLYEADPDSATKTPNNMNEP 120
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121 WKAVDTIADESFQYDLGRVWKINTEVRSFPGVRSFYLAFOYGGCMSLIAVRVY 180
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181 RRCPRRIIONGALFOETLSGAESTSLVAANGSCIANAEVDVPIKLYCNGDGEVLPIGR 240
241 MCKAGEAENVGVNCGCGSGTFKANOGEACTHCPINSTRITSEGTNCVCRNGYIRADL 300
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421 APSAASIMHOVSTVDSITLSMSQDPQNGVILIDYLOYTEKELSEYNATATKSPNTYT 480
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481 GLKAGAIYFOVARTVAGYGRYSGRMVOTMTEAEYOTSIQEKPLILIGSSAAGLVFLI 540
481 GLKAGAIYFOVARTVAGYGRYSGRMVOTMTEAEYOTSIQEKPLILIGSSAAGLVFLI 540
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541 AVVVAIVCNRRGFRADESEYTDKLOHYTSNGHTPGMKIYIDPFTYEDNEAVREFAKET 600
601 DISCVKIEOVIGAGEGECVSGHLKPGKREIFVAIKTLKSGYTEKORDFLEASIMGO 660
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721 LADMNVVHDLAARNILVNSLVCKVSDGLSFLDPTSDPTYSALGKFPRIWTAPE 780
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901 TYDEWELEATKMGQYKESFNAGTSPDVVSQMMEDILVGTALAHOKKILNSIOVMA 960
901 TYDEWELEATKMGQYKESFNAGTSPDVVSQMMEDILVGTALAHOKKILNSIOVMA 960
961 OMNOIQOSVEV 970
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RESULT 2
US-08-702-367A-11
Sequence 11, Application us/08702367A
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBM
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks

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STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702.367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367A-11

Query Match
Best Local Similarity 100.0%; Score 970; DB 2; Length 970;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LAAVEETLMDSTTVAELGMVHPSPGMEVSGYDENNTITRYOVANVFESSQNNMLR 60
1 LAAVEETLMDSTTVAELGMVHPSPGMEVSGYDENNTITRYOVANVFESSQNNMLR 60
61 TKRIRRGARHIVIMKFSVROCSSIPSPGSKETFNLYYEADDSATKTPNMENP 120
61 TKRIRRGARHIVIMKFSVROCSSIPSPGSKETFNLYYEADDSATKTPNMENP 120
61 TKRIRRGARHIVIMKFSVROCSSIPSPGSKETFNLYYEADDSATKTPNMENP 120
121 WKAVDTIADESFQYDLGRVWKINTEVRSFPGVRSFYLAFOYGGCMSLIAVRVY 180
121 WKAVDTIADESFQYDLGRVWKINTEVRSFPGVRSFYLAFOYGGCMSLIAVRVY 180
181 RRCPRRIIONGALFOETLSGAESTSLVAANGSCIANAEVDVPIKLYCNGDGEVLPIGR 240
181 RRCPRRIIONGALFOETLSGAESTSLVAANGSCIANAEVDVPIKLYCNGDGEVLPIGR 240
241 MCKAGEAENVGVNCGCGSGTFKANOGEACTHCPINSTRITSEGTNCVCRNGYIRADL 300
241 MCKAGEAENVGVNCGCGSGTFKANOGEACTHCPINSTRITSEGTNCVCRNGYIRADL 300
301 DPLDMCCTTIPSAPOAVISSVNETSLMLEMTPPRDSGREDLVYNTICKSCSGRGACTR 360
301 DPLDMCCTTIPSAPOAVISSVNETSLMLEMTPPRDSGREDLVYNTICKSCSGRGACTR 360
361 CGDNVOYAPROGLTEPRITISDLAHTQYTEIQAENVGTDOSSPSPQFASVNTITNOA 420
361 CGDNVOYAPROGLTEPRITISDLAHTQYTEIQAENVGTDOSSPSPQFASVNTITNOA 420
421 APSAASIMHOVSTVDSITLSMSQDPQNGVILIDYLOYTEKELSEYNATATKSPNTYT 480
421 APSAASIMHOVSTVDSITLSMSQDPQNGVILIDYLOYTEKELSEYNATATKSPNTYT 480
481 GLKAGAIYFOVARTVAGYGRYSGRMVOTMTEAEYOTSIQEKPLILIGSSAAGLVFLI 540
481 GLKAGAIYFOVARTVAGYGRYSGRMVOTMTEAEYOTSIQEKPLILIGSSAAGLVFLI 540
541 AVVVAIVCNRRGFRADESEYTDKLOHYTSNGHTPGMKIYIDPFTYEDNEAVREFAKET 600
541 AVVVAIVCNRRGFRADESEYTDKLOHYTSNGHTPGMKIYIDPFTYEDNEAVREFAKET 600
601 DISCVKIEOVIGAGEGECVSGHLKPGKREIFVAIKTLKSGYTEKORDFLEASIMGO 660
601 DISCVKIEOVIGAGEGECVSGHLKPGKREIFVAIKTLKSGYTEKORDFLEASIMGO 660
661 FDHPNVIHLEGVVTKSTPMIITEFMENGLDSFLRONDGOFTVIOVGLMGLGIAAGMKY 720

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Db 661 FDHPNVIHLEGVYTKSTPWIIITEFMENGLDSFLRQNDGQFTVIQVGMRLGIAAGMKY 720
Qy 721 LADMNVYHDLAARNILVNSNLCKVSDGLSRFLDDPTSDPTYSALGCKRPIMTAP 780
Db 721 LADMNVYHDLAARNILVNSNLCKVSDGLSRFLDDPTSDPTYSALGCKRPIMTAP 780
Qy 781 AIQYRKFTSASDVWSYGIYMEVMSYGERPYDMTNQDVINAIEDDYRLPPMDCPSALH 840
Db 781 AIQYRKFTSASDVWSYGIYMEVMSYGERPYDMTNQDVINAIEDDYRLPPMDCPSALH 840
Qy 841 QMLDCWQKDRNHRPKFGQIVNTLDKMINRPNLSKAMAPLSSGILNPLDRTIPDYTSFN 900
Db 841 QMLDCWQKDRNHRPKFGQIVNTLDKMINRPNLSKAMAPLSSGILNPLDRTIPDYTSFN 900
Qy 901 TYDEMLEAIKMGQYKESFANAGFTSFDVYSQMMEDILRVGYTLAGHOKKILNSIQVWRA 960
Db 901 TYDEMLEAIKMGQYKESFANAGFTSFDVYSQMMEDILRVGYTLAGHOKKILNSIQVWRA 960
Qy 961 QMNOIOSVEY 970
Db 961 QMNOIOSVEY 970

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RESULT 3

```

PCT-US95-04681-11
Sequence 11, Application PC/TUS9504681
GENERAL INFORMATION:

```

```

APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine
Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESS: Amgen Patent Operations/ABW
STREET: 1040 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SRO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-11

```

```

Query Match 100.0%; Score 970; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy 1 LAAVEETLNDSTTATATLGMVYHPPSGMREVSQYDENMNTITTYOVCNFBSSQNNMLR 60
Db 1 LAAVEETLNDSTTATATLGMVYHPPSGMREVSQYDENMNTITTYOVCNFBSSQNNMLR 60
Qy 61 TKFIRRGARHIVEMKFSYRDCSSIPSVGSCKETFNLYYVADPDSATKTPPNMEND 120
Db 61 TKFIRRGARHIVEMKFSYRDCSSIPSVGSCKETFNLYYVADPDSATKTPPNMEND 120
Qy 121 WNVVDITIADESFOVDLGRVAKINTEVRSFGVSRSGFYLAFOYGGCMLIAVREY 180

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Db 121 WNVVDITIADESFOVDLGRVAKINTEVRSFGVSRSGFYLAFOYGGCMLIAVREY 180
Qy 181 RCPRIIONGAIIEQETLSGAEASTSLVARGSCIANAEVDVPIKLYCNGDGEWLVP 240
Db 181 RCPRIIONGAIIEQETLSGAEASTSLVARGSCIANAEVDVPIKLYCNGDGEWLVP 240
Qy 241 MCKAGFEAVENGIVCRKCPSTGFANOGDEACTHCPINSRTSGATNCVCRCNGYTRADL 300
Db 241 MCKAGFEAVENGIVCRKCPSTGFANOGDEACTHCPINSRTSGATNCVCRCNGYTRADL 300
Qy 301 DPLMPCCTTIPSAPQAVISSVNETSLMLEWTPPHDSGREDLYNINICKSCGSGRAC 360
Db 301 DPLMPCCTTIPSAPQAVISSVNETSLMLEWTPPHDSGREDLYNINICKSCGSGRAC 360
Qy 361 CGDNVOYAPRQGLTERIRIYISDLAHTQYTFEIOAVNGVTDSPSPQFASVNIIT 420
Db 361 CGDNVOYAPRQGLTERIRIYISDLAHTQYTFEIOAVNGVTDSPSPQFASVNIIT 420
Qy 421 APSAVSIMHOVSRTVDSITLSMSQPDQPNQVILDYELQYKEKELSEYNATAIKSP 480
Db 421 APSAVSIMHOVSRTVDSITLSMSQPDQPNQVILDYELQYKEKELSEYNATAIKSP 480
Qy 481 GLKAGAIYFQVARRIVAGYGRYSGKMYFQMTAEAYOTSIOEKLPLIGSSAAGLVFL 540
Db 481 GLKAGAIYFQVARRIVAGYGRYSGKMYFQMTAEAYOTSIOEKLPLIGSSAAGLVFL 540
Qy 541 AVVYIAIVCNRRGERADSEYTKLOHYTSGHITTPGKIYIDPFTTEDNEAREPAKET 600
Db 541 AVVYIAIVCNRRGERADSEYTKLOHYTSGHITTPGKIYIDPFTTEDNEAREPAKET 600
Qy 601 DISCVKIEQVIGAGEFGEVCSGHLKPGKREIFVAKITLKSQYTERKORDPSEASIM 660
Db 601 DISCVKIEQVIGAGEFGEVCSGHLKPGKREIFVAKITLKSQYTERKORDPSEASIM 660
Qy 661 FDHPNVIHLEGVYTKSTPWIIITEFMENGLDSFLRQNDGQFTVIQVGMRLGIAAGMKY 720
Db 661 FDHPNVIHLEGVYTKSTPWIIITEFMENGLDSFLRQNDGQFTVIQVGMRLGIAAGMKY 720
Qy 721 LADMNVYHDLAARNILVNSNLCKVSDGLSRFLDDPTSDPTYSALGCKRPIMTAP 780
Db 721 LADMNVYHDLAARNILVNSNLCKVSDGLSRFLDDPTSDPTYSALGCKRPIMTAP 780
Qy 781 AIQYRKFTSASDVWSYGIYMEVMSYGERPYDMTNQDVINAIEDDYRLPPMDCPSALH 840
Db 781 AIQYRKFTSASDVWSYGIYMEVMSYGERPYDMTNQDVINAIEDDYRLPPMDCPSALH 840
Qy 841 QMLDCWQKDRNHRPKFGQIVNTLDKMINRPNLSKAMAPLSSGILNPLDRTIPDYTSFN 900
Db 841 QMLDCWQKDRNHRPKFGQIVNTLDKMINRPNLSKAMAPLSSGILNPLDRTIPDYTSFN 900
Qy 901 TYDEMLEAIKMGQYKESFANAGFTSFDVYSQMMEDILRVGYTLAGHOKKILNSIQVWRA 960
Db 901 TYDEMLEAIKMGQYKESFANAGFTSFDVYSQMMEDILRVGYTLAGHOKKILNSIQVWRA 960
Qy 961 QMNOIOSVEY 970
Db 961 QMNOIOSVEY 970

```

RESULT 4

```

US-08-542-635-2
Sequence 2, Application US/08542635
Patent No. 6218356
GENERAL INFORMATION:

```

```

APPLICANT: Pawson, Anthony
APPLICANT: Henkemeyer, Mark
APPLICANT: Letwin, Kenneth
TITLE OF INVENTION: NOVEL NEURAL RECEPTOR
TITLE OF INVENTION: TYROSINE KINASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESS: Bereskin & Parr

```

STREET: 40 King Street West, Box 401
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/542,635
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McDiarmid, Shona S.
REGISTRATION NUMBER: 38,798
REFERENCE/DOCKET NUMBER: 3153-162
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
TELEX: 06-23115
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Embryo
IMMEDIATE SOURCE:
LIBRARY: lambda gt10 cDNA library
CLONE: Combined pNukRACE A2 and K2 and cDNA clones
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Distal end of chromosome 4
MAP POSITION: near the and-1 mutation
US-08-542-635-2

Query Match 33.2%; Score 322; DB 4; Length 994;
Best Local Similarity 100.0%; Pred. No. 1.8e-286;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 159 GFYIAFDYGGCMLIAVRVYFRKCPRIIONGAIFQETLSAESTSVIARSGSIAAEE 218
DB 181 GFYIAFDYGGCMLIAVRVYFRKCPRIIONGAIFQETLSAESTSVIARSGSIAAEE 240
QY 219 VDVPIKLYCNGDGMVLPDGRCKMKGFEAVENGTVRCGSPGTFKANOGEACTHCPIN 278
DB 241 VDVPIKLYCNGDGMVLPDGRCKMKGFEAVENGTVRCGSPGTFKANOGEACTHCPIN 300
QY 279 SRTSEGAATNCVCRNGYRRADLDLDMPCCTTIPSAPOAVISVNETSLMLFMTPPRDSG 338
DB 301 SRTSEGAATNCVCRNGYRRADLDLDMPCCTTIPSAPOAVISVNETSLMLFMTPPRDSG 360
QY 339 REDLYNITICSCSGGRACRCCDNOYARROIGNEPRIYISDLAHTQYTEIOAVN 398
DB 361 REDLYNITICSCSGGRACRCCDNOYARROIGNEPRIYISDLAHTQYTEIOAVN 420
QY 399 GVTDOSPSPQFASVNTITNOAASAVSIMHVSRTVDSITLSMSOPDQNGVILDYELQ 458
DB 421 GVTDOSPSPQFASVNTITNOAASAVSIMHVSRTVDSITLSMSOPDQNGVILDYELQ 480
QY 459 YYEKELSEYNATAIKSPNTVT 480
DB 481 YYEKELSEYNATAIKSPNTVT 502

RESULT 5
US-08-162-809-18
Sequence 18, Application US/08162809

Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydon G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 995 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-809-18

Query Match 10.6%; Score 103; DB 1; Length 995;
Best Local Similarity 100.0%; Pred. No. 6.5e-86;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 574 TPGMKIYIDPFTYEDNEAVREFAKTIDISCVKIEQVITAGEFGEVCSGHLTPKREIF 633
DB 599 TPGMKIYIDPFTYEDNEAVREFAKTIDISCVKIEQVITAGEFGEVCSGHLTPKREIF 658
QY 634 VAKTKLSGTEKORDPLSEASIMGQFDHPNYIHLEGVTKS 676
DB 659 VAKTKLSGTEKORDPLSEASIMGQFDHPNYIHLEGVTKS 701

RESULT 6
US-08-673-789-5
Sequence 5, Application US/08673789
Patent No. 5814479
GENERAL INFORMATION:
APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 995
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
US-08-673-789-5

Query Match 10.6%; Score 103; DB 2; Length 995;

Best Local Similarity 100.0%; Pred. No. 6,5e-86;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEGVCSGHLKLPGRKEIF 633
DB 599 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEGVCSGHLKLPGRKEIF 658
QY 634 VAIKTLKSGYTEKORRPLESEASIMGQFDHPNVIHLEGVYTKS 676
DB 659 VAIKTLKSGYTEKORRPLESEASIMGQFDHPNVIHLEGVYTKS 701

RESULT 7

US-08-162-809-12
Sequence 12, Application US/08162809
Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
City: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1011 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-809-12

Query Match 10.6%; Score 103; DB 1; Length 1011;

Best Local Similarity 100.0%; Pred. No. 6,6e-86;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEGVCSGHLKLPGRKEIF 633
DB 615 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEGVCSGHLKLPGRKEIF 674
QY 634 VAIKTLKSGYTEKORRPLESEASIMGQFDHPNVIHLEGVYTKS 676
DB 675 VAIKTLKSGYTEKORRPLESEASIMGQFDHPNVIHLEGVYTKS 717

RESULT 8

US-08-449-645A-17
Sequence 17, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
City: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-17

Query Match 4.1%; Score 40; DB 2; Length 998;

Best Local Similarity 100.0%; Pred. No. 3,2e-28;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 RWTAPFAIOYRKFTSASDVSYGIVMVEVSYGRRPYMDM 814
DB 801 RWTAPFAIOYRKFTSASDVSYGIVMVEVSYGRRPYMDM 840

RESULT 9

US-08-702-367A-17
Sequence 17, Application US/08702367A
Patent No. 5981246

GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367A-17

Query Match 4.1%; Score 40; DB 2; Length 998;
Best Local Similarity 100.0%; Pred. No. 3.2e-28;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 814
|||||
DB 801 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 840

RESULT 10
PCT-US95-04681-17
Sequence 17, Application PC/TUS9504681
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-17

Query Match 4.1%; Score 40; DB 5; Length 998;
Best Local Similarity 100.0%; Pred. No. 3.2e-28;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 814
|||||
DB 801 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 840

RESULT 11
PCT-US96-00419-2
Sequence 2, Application PC/TUS9600419
GENERAL INFORMATION:
APPLICANT: Thomas Closssek, Axel Ullrich, Birgit
ATTORNEY/AGENT INFORMATION:
NAME: Millaer
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00419
FILING DATE: January 3, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA: Including application
PRIOR APPLICATION DATA: described below
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 998
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-00419-2

Query Match 4.1%; Score 40; DB 5; Length 998;
Best Local Similarity 100.0%; Pred. No. 3.2e-28;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 814
|||||
DB 801 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 840

RESULT 12
US-08-222-616-25

Sequence 25, Application US/08222616
Patent No. 5635177
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patln (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,616
FILING DATE: 4-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-222-616-25

Query Match 4.0%; Score 39; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.2e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 ARNLVNSNLVCKVSDGLSRFLEDDTSDPTYSALGK 771
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Db 1 ARNLVNSNLVCKVSDGLSRFLEDDTSDPTYSALGK 39

RESULT 13
PCT-US95-04228-25
Sequence 25, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patln (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-04228-25

Query Match 4.0%; Score 39; DB 5; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.2e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 ARNLVNSNLVCKVSDGLSRFLEDDTSDPTYSALGK 771
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Db 1 ARNLVNSNLVCKVSDGLSRFLEDDTSDPTYSALGK 39

RESULT 14
US-08-456-647B-10
Sequence 10, Application US/08456647B
Patent No. 5811516
GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,647B
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07251/007002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-647B-10

Query Match 3.8%; Score 37; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 NILVNSNLVCKVSDRGLSRFLEDDTSDPTYTSALGK 771
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DB 1 NILVNSNLVCKVSDRGLSRFLEDDTSDPTYTSALGK 37

RESULT 15
US-08-237-401A-10
Sequence 10, Application US/08237401A
Patent No. 5637448
GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Halle Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-237-401A-10

Query Match 3.8%; Score 37; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 NILVNSNLVCKVSDRGLSRFLEDDTSDPTYTSALGK 771

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DB 1 NILVNSNLVCKVSDRGLSRFLEDDTSDPTYTSALGK 37

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Wed Jul 25 13:03:50 2001

us-09-378-759-11.oli.rai

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:32:19 ; Search time 53.59 Seconds
(without alignments)
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Title: US-09-378-759-11

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Sequence: 1 LLAAYEETLMDSTTATAEIG.....IINSIQVMRAQNMQISVEV 970

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Word size: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	970	100.0	970	11	US-08-702-367-11
3	970	100.0	970	17	US-09-378-759-11
4	490	50.5	524	11	US-08-730-700A-7
5	322	33.2	994	6	US-08-235-407-2
6	322	33.2	984	11	US-08-727-463-2
7	322	33.2	984	11	US-08-727-463-2
8	322	33.2	994	11	US-08-730-700-2
9	322	33.2	994	11	US-08-730-700A-2
10	198	20.4	551	23	US-60-206-600-138

11	198	20.4	551	23	US-60-208-965-196	Sequence 196, App
12	111	11.4	191	23 <td>US-60-233-606-78</td> <td>Sequence 78, App</td>	US-60-233-606-78	Sequence 78, App
13	98	10.1	162	23 <td>US-60-248-798-295</td> <td>Sequence 295, App</td>	US-60-248-798-295	Sequence 295, App
14	83	8.6	143	23 <td>US-60-160-202-4014</td> <td>Sequence 4014, App</td>	US-60-160-202-4014	Sequence 4014, App
15	83	8.6	84	23 <td>US-60-160-209-3395</td> <td>Sequence 3395, App</td>	US-60-160-209-3395	Sequence 3395, App
16	83	8.6	149	23 <td>US-60-169-868-4968</td> <td>Sequence 4968, App</td>	US-60-169-868-4968	Sequence 4968, App
17	83	8.6	173	23 <td>US-60-196-713-3263</td> <td>Sequence 3263, App</td>	US-60-196-713-3263	Sequence 3263, App
18	83	8.6	179	23 <td>US-60-187-380-108</td> <td>Sequence 108, App</td>	US-60-187-380-108	Sequence 108, App
19	83	8.6	179	23 <td>US-60-187-412-3971</td> <td>Sequence 3971, App</td>	US-60-187-412-3971	Sequence 3971, App
20	82	8.5	83	23 <td>US-60-160-202-4070</td> <td>Sequence 4070, App</td>	US-60-160-202-4070	Sequence 4070, App
21	82	8.5	83	23 <td>US-60-160-202-4085</td> <td>Sequence 4085, App</td>	US-60-160-202-4085	Sequence 4085, App
22	65	6.7	84	23 <td>US-60-202-183-289</td> <td>Sequence 289, App</td>	US-60-202-183-289	Sequence 289, App
23	51	5.3	69	23 <td>US-60-192-733-3058</td> <td>Sequence 3058, App</td>	US-60-192-733-3058	Sequence 3058, App
24	51	5.3	69	23 <td>US-60-194-091-1122</td> <td>Sequence 1122, App</td>	US-60-194-091-1122	Sequence 1122, App
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27	42	4.3	48	23 <td>US-60-162-245-2293</td> <td>Sequence 2293, App</td>	US-60-162-245-2293	Sequence 2293, App
28	41	4.2	41	23 <td>US-60-163-233-3570</td> <td>Sequence 3570, App</td>	US-60-163-233-3570	Sequence 3570, App
29	41	4.2	44	23 <td>US-60-205-167-143</td> <td>Sequence 143, App</td>	US-60-205-167-143	Sequence 143, App
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33	40	4.1	529	11 <td>US-08-730-700A-11</td> <td>Sequence 11, App</td>	US-08-730-700A-11	Sequence 11, App
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42	39	4.0	59	8 <td>US-08-446-648-25</td> <td>Sequence 25, App</td>	US-08-446-648-25	Sequence 25, App
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ALIGNMENTS

RESULT 1
US-08-449-645-11
Sequence 11, Application US/08449645
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
APPLICANT: Welch, Andrew A.
APPLICANT: Jing, Shugian
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645
FILING DATE: May 24, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287-A
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
us-08-449-645-11

Query Match 100.0%; Score 970; DB 8; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 481 GLKAGALYVQVARTVAGYGRYSKAMFQTMTEAEYQTSIOEKLPLITIGSSAAGLVFLI 540
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QY 961 QMNOIOSVEV 970
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DB 961 QMNOIOSVEV 970

RESULT 2

us-08-702-367-11
Sequence 11, Application US/08702367

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,367

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/229, 509

FILING DATE: 15-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 970 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

us-08-702-367-11

Query Match 100.0%; Score 970; DB 11; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 601 DISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDPFLSEASIMQ 660
Qy 661 FDHPNVIHLEGVYTKSTPMIITTEFMENGSLDSFLRQNDGQFTYVQLVGMRLGIAAGKY 720
Db 661 FDHPNVIHLEGVYTKSTPMIITTEFMENGSLDSFLRQNDGQFTYVQLVGMRLGIAAGKY 720
Qy 721 LADMYVHRLDLAARNILVNSNLVCKVSDFGLSRFLLEDTSPTYSALGKFPIRMATAPE 780
Db 721 LADMYVHRLDLAARNILVNSNLVCKVSDFGLSRFLLEDTSPTYSALGKFPIRMATAPE 780
Qy 781 AIQYRKFTSASDVWSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLPRPMDCPALH 840
Db 781 AIQYRKFTSASDVWSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLPRPMDCPALH 840
Qy 841 QLMDCWOKDRNHRPKFGQIYVNTLDKMIARNPNSLKAMAPLSSGINPLDRTIDYTSFN 900
Db 841 QLMDCWOKDRNHRPKFGQIYVNTLDKMIARNPNSLKAMAPLSSGINPLDRTIDYTSFN 900
Qy 901 TVDEWLEAIKMGQYKESFANAGTSPFDVVSQMMEDILRVGVTLAGHOKKLINSIQWRA 960
Db 901 TVDEWLEAIKMGQYKESFANAGTSPFDVVSQMMEDILRVGVTLAGHOKKLINSIQWRA 960
Qy 961 OMNIOSEYV 970
Db 961 OMNIOSEYV 970

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; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
us-09-378-759-11

Query Match      100.0%; Score 970; DB 17; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLAVEETLMDSTATATLEGMVHPSPGWEVSGYDNNMTIRTYOCNPFESSONMLR 60
Db 1 LLAVEETLMDSTATATLEGMVHPSPGWEVSGYDNNMTIRTYOCNPFESSONMLR 60
Qy 61 TKFIRRGARHRIHEMKEFSVRDCSSIPSPGCKEFPNLYYEADFDSATKTPNNMNEP 120
Db 61 TKFIRRGARHRIHEMKEFSVRDCSSIPSPGCKEFPNLYYEADFDSATKTPNNMNEP 120
Qy 121 WVKVDTTAADESPQVDLGRVMAKINTEVRSFGVRSNGFYLAPODYGCMSLIAVREY 180
Db 121 WVKVDTTAADESPQVDLGRVMAKINTEVRSFGVRSNGFYLAPODYGCMSLIAVREY 180
Qy 181 RCPRIIONCAIFOETLGAESTILVARGSCIANEEVDPYIKLYCNGDGEMLVPIGRC 240
Db 181 RCPRIIONCAIFOETLGAESTILVARGSCIANEEVDPYIKLYCNGDGEMLVPIGRC 240
Qy 241 MCRAGEFAVENGTVCRCGSPGTEKANGDCACTHCPINSTRTSEGATNCCRNNGYRADL 300
Db 241 MCRAGEFAVENGTVCRCGSPGTEKANGDCACTHCPINSTRTSEGATNCCRNNGYRADL 300
Qy 301 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDGGGRDLVYNTICSGSGRGACTR 360
Db 301 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDGGGRDLVYNTICSGSGRGACTR 360
Qy 361 CGDNVOYARQLGTEPRRIYISDLAHTQYTELQAVKVTQSPSPQFASVNTTNOA 420
Db 361 CGDNVOYARQLGTEPRRIYISDLAHTQYTELQAVKVTQSPSPQFASVNTTNOA 420
Qy 421 APSAVSIMHOVSRTVDSITLSMSQDPQNGVILIDYELQYEREKELSEYNATAKSPNTVT 480
Db 421 APSAVSIMHOVSRTVDSITLSMSQDPQNGVILIDYELQYEREKELSEYNATAKSPNTVT 480
Qy 481 GLKAGAIYFOVARTVAGYGRSGKMYFQMTAEAYOTSIQEKPLIIGSSAAGLVFLI 540
Db 481 GLKAGAIYFOVARTVAGYGRSGKMYFQMTAEAYOTSIQEKPLIIGSSAAGLVFLI 540
Qy 541 AVVVAIAYCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFYEDPNEAVREFAKEI 600
Db 541 AVVVAIAYCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFYEDPNEAVREFAKEI 600
Qy 601 DISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDPFLSEASIMQ 660
Db 601 DISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDPFLSEASIMQ 660
Qy 661 FDHPNVIHLEGVYTKSTPMIITTEFMENGSLDSFLRQNDGQFTYVQLVGMRLGIAAGKY 720
Db 661 FDHPNVIHLEGVYTKSTPMIITTEFMENGSLDSFLRQNDGQFTYVQLVGMRLGIAAGKY 720
Qy 721 LADMYVHRLDLAARNILVNSNLVCKVSDFGLSRFLLEDTSPTYSALGKFPIRMATAPE 780
Db 721 LADMYVHRLDLAARNILVNSNLVCKVSDFGLSRFLLEDTSPTYSALGKFPIRMATAPE 780
Qy 781 AIQYRKFTSASDVWSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLPRPMDCPALH 840
Db 781 AIQYRKFTSASDVWSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLPRPMDCPALH 840
Qy 841 QLMDCWOKDRNHRPKFGQIYVNTLDKMIARNPNSLKAMAPLSSGINPLDRTIDYTSFN 900
Db 841 QLMDCWOKDRNHRPKFGQIYVNTLDKMIARNPNSLKAMAPLSSGINPLDRTIDYTSFN 900

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RESULT 3

US-09-378-759-11

Sequence 11, Application US/09378759

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Denavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/378,759

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/702,367

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

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Db      215 FDBPWNVTHLESGYVTSSTVYMLITTEFMENSSLDSEFLNQNGOGFTVLQVLGMLRGTAAGIKY   274
Qy      721 LADNVYHVDLAAARNILVNLSNLVCXVSDFGLSRPLEDDTSDPTTYSALGKFPRTWPAE   780
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Db      275 LADNVYHVDLAAARNILVNLSNLVCXVSDFGLSRPLEDDTSDPTTYSALGKFPRTWPAE   334
Qy      781 AIOYRRETSASDWSYGIVVMENEVSYSGRPYWDXTNODVINATEODRYLPPEMDCPSALH   840
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Db      335 AIOYRRETSASDWSYGIVVMENEVSYSGRPYWDXTNODVINATEODRYLPPEMDCPSALH   394
Qy      901 TYVEWYLEATKMCOYKISFANAGFTSPDVVSOOMMEDILRVGYTLAIGHOKKLINSIQVRA   966
       |||
Db      455 TYVEWYLEATKMCOYKISFANAGFTSPDVVSOOMMEDILRVGYTLAIGHOKKLINSIQVRA   514
Qy      961 QMNQIOSVEY 970
       |||
Db      515 QMNQIOSVEY 524

RESULT      5
US-08-235-407-2
Sequence 2, Application US/08235407
GENERAL INFORMATION:
APPLICANT: Pawson, Anthony
APPLICANT: Henkemeyer, Mark
APPLICANT: Letwin, Kenneth
TITLE OF INVENTION: NOVEL NEURAL KINASE AND RECEPTOR
TITLE OF INVENTION: TYROSINE KINASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West, Box 401
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,407
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: kurdyyak, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-82
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
TELEX: 06-23115
INFORMATION FOR SEQ. ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Embryo
IMMEDIATE SOURCE:
LIBRARY: lambda gtl0 cDNA library
CLONE: Combined pNUKRACE A2 and K2 and cDNA clones
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Distal end of chromosome 4
MAP POSITION: near the amd-1 mutation

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US-08-235-407-2

Query Match	33.2%	Score 322;	DB 6;	Length 994;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 322;	Conservative	0;	Mismatches	0; Indels

Oy	159	GFYLAFOYGGCMSLIANVRVYRRCPRITONGAIFQETLSGAESTSLVARGSCINAAE	218
Db	181	GFYLAFOYGGCMSLIANVRVYRRCPRITONGAIFQETLSGAESTSLVARGSCINAAE	240
Oy	219	VDVPILKLYCNGDGMVLVPYIGCMCKAGEAVENTGTCVRCGCBSTFKANGCDEACTHCPIN	278
Db	241	VDVPILKLYCNGDGMVLVPYIGCMCKAGEAVENTGTCVRCGCBSTFKANGCDEACTHCPIN	300
Oy	279	SRTTSECATNCVCNRNGXYRALDPLDLMDCCTTIPSAPOAVISVSVETSLMLEMTPPBRSGG	338
Db	301	SRTTSECATNCVCNRNGXYRALDPLDLMDCCTTIPSAPOAVISVSVETSLMLEMTPPBRSGG	360
Oy	339	REDLYNYITICKSCGSGRACRTCGDNDQYAPROLGLTEPRITYSIDLAAHYTFEIOAVN	398
Db	361	REDLYNYITICKSCGSGRACRTCGDNDQYAPROLGLTEPRITYSIDLAAHYTFEIOAVN	420
Oy	399	GVTDOSPSPQFASYNITITNNOAASAVSISIMQVSRVDSITLSWSQDPQNGVILDELO	458
Db	421	GVTDOSPSPQFASYNITITNNOAASAVSISIMQVSRVDSITLSWSQDPQNGVILDELO	480
Oy	459	YYEKELSEYNATAIKSPNTYVT	480
Db	481	YYEKELSEYNATAIKSPNTYVT	502

RESULT 6
US-08-727-463-2

; Sequence 2, Application US/08727463
; GENERAL INFORMATION:

:
:
: APPLICANT: Pawson, Anthony
: APPLICANT: Henkemeyer, Mark
: APPLICANT: Letvin, Kenneth
: TITLE OF INVENTION: NEURAL RECEPTOR TYROSINE KINASES
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:

ADDRESSEE: MERCHANT & GOULD
STREET: 3100 Northwest Center, 90 South Seventh Street
CITY: Minneapolis

STATE: Minnesota
COUNTRY: U.S.A.
ZIP: 55403-4131

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: Patientin Release #1.0, Version #1.25
6  CURRENT APPLICATION NAME:

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: CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/727,463
 : FILING DATE: 18-OCT-1996

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: M&G 7933.89-US-WO
TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 332-5300
TELEFAX: (612) 332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 994 amino acid
TYPE: amino acid
STRANDEDNESS: single

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:   TOPOLOGY: linear
:   MOLECULE TYPE: protein
:   ORIGINAL SOURCE:
:   ORGANISM: Mus musculus

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DEVELOPMENTAL STAGE: Embryo
IMMEDIATE SOURCE:

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US-08-727-463-2

Query Match	33.2%	Score 322;	DB 11;	Length 994;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 322: Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Oy	159	GFYLAFDQYGGCSMLIAVREYRCPILIONGALFOETLSGAESTSLVARGSCINAAE	218
Db	181	GFYLAFDQYGGCSMLIAVREYRCPILIONGALFOETLSGAESTSLVARGSCINAAE	240
Oy	219	VDVPIKILYCNDEGMVLVPIGRMCKAGFEAVENGSTVCRCGSPGTFKRNQDDEACTHCIPIN	278
Db	241	VDVPIKILYCNDEGMVLVPIGRMCKAGFEAVENGSTVCRCGSPGTFKRNQDDEACTHCIPIN	300
Oy	279	SRTSSEGATNCVCNENGYRADLDLDLDMPCITTIPSAPOAVISVNETSLMLEMTPPRDSCG	338
Db	301	SRTSSEGATNCVCNENGYRADLDLDLDMPCITTIPSAPOAVISVNETSLMLEMTPPRDSCG	360
Oy	339	REDLYVNIICKSCSGGRACITRCGDNNQYAPROLGLTEPRITYSDDLANTQYTFEIOAVN	398
Db	361	REDLYVNIICKSCSGGRACITRCGDNNQYAPROLGLTEPRITYSDDLANTQYTFEIOAVN	420
Oy	399	GVTQSPSPQFASVNIITTNQAAASAVSIMHQVSRVDSITLSWSQPDQNGVILDELO	458
Db	421	GVTQSPSPQFASVNIITTNQAAASAVSIMHQVSRVDSITLSWSQPDQNGVILDELO	480
Oy	459	YXEKELSEYNATIAKSPNTIYT	480
Db	481	YXEKELSEYNATIAKSPNTIYT	502

RESULT 7
HS-08-727-

Sequence 2, Application US/08727463A
GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: PAMSON, ANTHONY
APPLICANT: HENKEMEYER, MARK
APPLICANT: LETWIN, KENNETH
APPLICANT: MOUNT SINAI HOSPITAL CORPORATION
TITLE OF INVENTION: METHODS FOR IDENTIFYING SUBSTANCES AFFECTING RECEPTOR
TITLE OF INVENTION: TYROSINE KINASE ACTIVITY (AS AMENDED)
INVENTOR: PAMSON, ANTHONY

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; FILE REFERENCE: 7933.09
; CURRENT APPLICATION NUM
; CURRENT FILING DATE: 19
; EARLIER APPLICATION NUM

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NUMBER OF ST

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; NUMBER OF SEQ ID NOS: 4
;
; SOFTWARE: PatentIn Ver.
;
; SEQ ID NO 2
;
; LENGTH: 994
;
; TYPE: PRT
;
; ORGANISM: Mus musculus

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US-08-727-463-2
ANALYSIS: 100% MATCHES
Query Match      33.2%; Score 322; DB 11; Length 994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps
0y 159 GGYTAAFDYGGCMSLIAVRVYRRCPCRIQNGAIFQETLSAESTSLVAARGSCINAAEE 218
db 181 GGYTAAFDYGGCMSLIAVRVYRRCPCRIQNGAIFQETLSAESTSLVAARGSCINAAEE 240

```

QY 219 VDVPIKLYCNGDEMLVPIGRCKMKGFEAVENGTCVRCGPGSTFRKANGDEACTHCPIP 278
DB 241 VDVPIKLYCNGDEMLVPIGRCKMKGFEAVENGTCVRCGPGSTFRKANGDEACTHCPIP 300
QY 279 SRTTSGATNCVCRNGYRRADLPDLPCTTISAPQAVISSVNETSLMEWTPPRDSG 338
DB 301 SRTTSGATNCVCRNGYRRADLPDLPCTTISAPQAVISSVNETSLMEWTPPRDSG 360
QY 339 REDLVYNIICKSCGSGRACTRCGDNVQYAPRQLGLTEPRIVISDLAHTQYTFEIOAVN 398
DB 361 REDLVYNIICKSCGSGRACTRCGDNVQYAPRQLGLTEPRIVISDLAHTQYTFEIOAVN 420
QY 399 GVTDSPEFSPQFASVNTTNOAPSAVSIMHOVSRVDSITLSMSQPDQPNVILDYELQ 458
DB 421 GVTDSPEFSPQFASVNTTNOAPSAVSIMHOVSRVDSITLSMSQPDQPNVILDYELQ 480
QY 459 YYEKELSEYNATAIKSPNTVT 480
DB 481 YYEKELSEYNATAIKSPNTVT 502

RESULT 8
US-08-730-700-2
; Sequence 2, Application US/08730700
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; TITLE OF INVENTION: Method of Activating a Novel Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bereskin & Parr
; STREET: 40 King Street West, Box 401
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,700
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurydyk, Linda M.
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; TELEX: 06-23115
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Embryo
; IMMEDIATE SOURCE:
; LIBRARY: lambda gt10 cDNA library
; CLONE: Combined pmurace A2 and K2 and cDNA clones
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Distal end of chromosome 4
; MAP POSITION: near the abd-1 mutation
US-08-730-700-2

Query Match 33.2%; Score 322; DB 11; Length 994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 GFLYAFQDYGCKSLIAVRYFRKCPRIIONGAIFOETISGAESTSLVAARGSCIANAE 218
DB 181 GFLYAFQDYGCKSLIAVRYFRKCPRIIONGAIFOETISGAESTSLVAARGSCIANAE 240
QY 219 VDVPIKLYCNGDEMLVPIGRCKMKGFEAVENGTCVRCGPGSTFRKANGDEACTHCPIP 278
DB 241 VDVPIKLYCNGDEMLVPIGRCKMKGFEAVENGTCVRCGPGSTFRKANGDEACTHCPIP 300
QY 279 SRTTSGATNCVCRNGYRRADLPDLPCTTISAPQAVISSVNETSLMEWTPPRDSG 338
DB 301 SRTTSGATNCVCRNGYRRADLPDLPCTTISAPQAVISSVNETSLMEWTPPRDSG 360
QY 339 REDLVYNIICKSCGSGRACTRCGDNVQYAPRQLGLTEPRIVISDLAHTQYTFEIOAVN 398
DB 361 REDLVYNIICKSCGSGRACTRCGDNVQYAPRQLGLTEPRIVISDLAHTQYTFEIOAVN 420
QY 399 GVTDSPEFSPQFASVNTTNOAPSAVSIMHOVSRVDSITLSMSQPDQPNVILDYELQ 458
DB 421 GVTDSPEFSPQFASVNTTNOAPSAVSIMHOVSRVDSITLSMSQPDQPNVILDYELQ 480
QY 459 YYEKELSEYNATAIKSPNTVT 480
DB 481 YYEKELSEYNATAIKSPNTVT 502

RESULT 9
US-08-730-700A-2
; Sequence 2, Application US/08730700A
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; TITLE OF INVENTION: Method of Activating a Novel Ligand
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Room 970
; STREET: 600 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1K5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,700A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,518
; FILING DATE: 13-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurydyk, Linda M.
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 416-586-3235
; TELEFAX: 416-586-3110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-730-700A-2

Query Match 33.2%; Score 322; DB 11; Length 994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

159 GFYLAFOYDYGCGSLAVRVYRKCPRIIONGAIFQETLSGAEISTLVAAAGSCIANAE 218
181 GFYLAFOYDYGCGSLAVRVYRKCPRIIONGAIFQETLSGAEISTLVAAAGSCIANAE 240
219 VDPVPIKLYCGDGMVLVPIRCMKAGFEAVENGTVRGCPGSGFKNODGACTHCPIN 278
241 VDPVPIKLYCGDGMVLVPIRCMKAGFEAVENGTVRGCPGSGFKNODGACTHCPIN 300
279 SRTSEGATNCVGNNGYRRADLDPLDMPCTTIPSAPOAVISSVNETSLMEMPDPDSCG 338
301 SRTSEGATNCVGNNGYRRADLDPLDMPCTTIPSAPOAVISSVNETSLMEMPDPDSCG 360
339 REDLVYNIICKSCGSGGACTRCGDNVQVAPROLGLTEPRIYISDLAHQYTFEIOAVN 398
361 REDLVYNIICKSCGSGGACTRCGDNVQVAPROLGLTEPRIYISDLAHQYTFEIOAVN 420
399 GVTQSPSPFQFASVNTTNOAPSAVSIMHQVSRVDSITLSMSPDOPNGVILDYELQ 458
421 GVTQSPSPFQFASVNTTNOAPSAVSIMHQVSRVDSITLSMSPDOPNGVILDYELQ 480
459 YEKELSEYNATAIKSPNTVT 480
481 YEKELSEYNATAIKSPNTVT 502

RESULT 10
US-60-206-600-138
; Sequence 138, Application US/60206600
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
; FILE REFERENCE: CL000627
; CURRENT APPLICATION NUMBER: US/60/206, 600
; CURRENT FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 551
; TYPE: PRF
; ORGANISM: HUMAN
US-60-206-600-138

Query Match 20.4%; Score 198; DB 23; Length 551;
Best Local Similarity 100.0%; Pred. No. 1.9e-199;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

574 TPQMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKPGKREIF 633
157 TPQMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKPGKREIF 216
634 VAIKTLKSGYTERKORRDLSEASIMGQFDPHPNVHLEGVTKSTPVMIITEFMENGSLDS 693
217 VAIKTLKSGYTERKORRDLSEASIMGQFDPHPNVHLEGVTKSTPVMIITEFMENGSLDS 276
694 FLRNDGQFTYIOLVGMRLGIAAGMKYLAADNMYVHRDLAARNILVNSMLVCKVSDGFLSR 753
277 FLRNDGQFTYIOLVGMRLGIAAGMKYLAADNMYVHRDLAARNILVNSMLVCKVSDGFLSR 336
754 FLEDDTSDPTYTSALGSK 771
337 FLEDDTSDPTYTSALGSK 354

RESULT 11
US-60-208-965-196

; Sequence 196, Application US/60208965
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
; FILE REFERENCE: CL000639
; CURRENT APPLICATION NUMBER: US/60/208, 965
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 551
; TYPE: PRF
; ORGANISM: HUMAN
US-60-208-965-196

Query Match 20.4%; Score 198; DB 23; Length 551;
Best Local Similarity 100.0%; Pred. No. 1.9e-199;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

574 TPQMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKPGKREIF 633
157 TPQMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKPGKREIF 216
634 VAIKTLKSGYTERKORRDLSEASIMGQFDPHPNVHLEGVTKSTPVMIITEFMENGSLDS 693
217 VAIKTLKSGYTERKORRDLSEASIMGQFDPHPNVHLEGVTKSTPVMIITEFMENGSLDS 276
694 FLRNDGQFTYIOLVGMRLGIAAGMKYLAADNMYVHRDLAARNILVNSMLVCKVSDGFLSR 753
277 FLRNDGQFTYIOLVGMRLGIAAGMKYLAADNMYVHRDLAARNILVNSMLVCKVSDGFLSR 336
754 FLEDDTSDPTYTSALGSK 771
337 FLEDDTSDPTYTSALGSK 354

RESULT 12
US-60-233-606-78
; Sequence 78, Application US/60233606
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
; FILE REFERENCE: CL000821
; CURRENT APPLICATION NUMBER: US/60/233, 606
; CURRENT FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 191
; TYPE: PRF
; ORGANISM: HUMAN
US-60-233-606-78

Query Match 11.4%; Score 111; DB 23; Length 191;
Best Local Similarity 100.0%; Pred. No. 4.9e-108;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

773 PIRMTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNOVYINAEIDYRLPP 832
5 PIRMTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNOVYINAEIDYRLPP 64
833 MDCPSALHQLMLDCMOKDRNHRPKFGQIVNTLDMKIRPNLSLKAAPLSSG 883
65 MDCPSALHQLMLDCMOKDRNHRPKFGQIVNTLDMKIRPNLSLKAAPLSSG 115

RESULT 13

```
US-60-248-798-295
; Sequence 295, Application US/60248798
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1000945
; CURRENT APPLICATION NUMBER: US/60/248,798
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 552
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 162
; TYPE: PRT
; ORGANISM: human
US-60-248-798-295
```

```
Query Match      10.1%; Score 98; DB 23; Length 162;
Best Local Similarity 100.0%; Pred. No. 2.2e-94;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 773 PIRMTAPEAIQYRKFTSASDVMSYGIYMEVMSYGERPYMDMTNODVYNAIEDYRLPPP 832
DB 65 PIRMTAPEAIQYRKFTSASDVMSYGIYMEVMSYGERPYMDMTNODVYNAIEDYRLPPP 124
OY 833 MDCPSALHQLMDCWQDRNRHRRPFGQIVNTLKMIRN 870
DB 125 MDCPSALHQLMDCWQDRNRHRRPFGQIVNTLKMIRN 162
```

```
RESULT 14
US-60-160-202-4014
; Sequence 4014, Application US/60160202
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
; FILE REFERENCE: C1000114
; CURRENT APPLICATION NUMBER: US/60/160,202
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 4392
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4014
; LENGTH: 84
; TYPE: PRT
; ORGANISM: HUMAN
US-60-160-202-4014
```

```
Query Match      8.6%; Score 83; DB 23; Length 84;
Best Local Similarity 100.0%; Pred. No. 8.1e-79;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 614 GEGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLSEASIMGQFDPNVIHLEGVY 673
DB 2 GEGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLSEASIMGQFDPNVIHLEGVY 61
OY 674 TKSTPVMITTEFMENGLSDSFLR 696
DB 62 TKSTPVMITTEFMENGLSDSFLR 84
```

```
RESULT 15
US-60-160-209-3995
; Sequence 3995, Application US/60160209
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES
; FILE REFERENCE: C1000113
```

```
; CURRENT APPLICATION NUMBER: US/60/160,209
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 4646
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3995
; LENGTH: 94
; TYPE: PRT
; ORGANISM: HUMAN
US-60-160-209-3995
```

```
Query Match      8.6%; Score 83; DB 23; Length 94;
Best Local Similarity 100.0%; Pred. No. 9e-79;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 614 GEGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLSEASIMGQFDPNVIHLEGVY 673
DB 2 GEGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLSEASIMGQFDPNVIHLEGVY 61
OY 674 TKSTPVMITTEFMENGLSDSFLR 696
DB 62 TKSTPVMITTEFMENGLSDSFLR 84
```

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Search completed: July 24, 2001, 16:34:52
Job time: 153 sec
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Wed Jul 25 13:03:51 2001

us-09-378-759-11.oli.rapm

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Db      361 CGDNVOYAPRQLGLEBRIYISDLAHTQYFETIOAVNGVTIDQSPFSPQFASVNTITNOA 420
QY      421 APSVSIIMHOVSRTVDSTITLSMSQPDQPNQIILDEYELQYKEKLESENNATLAKSPITVT 480
      |||||||
Db      421 APSVSIIMHOVSRTVDSTITLSMSQPDQPNQIILDEYELQYKEKLESENNATLAKSPITVT 480
QY      481 GLKAGAIYFQVRRATVAGYGRYSGKMYFQMTAEAYQTSIOEPLPLITGSSAAGLVFLI 540
      |||||||
Db      481 GLKAGAIYFQVRRATVAGYGRYSGKMYFQMTAEAYQTSIOEPLPLITGSSAAGLVFLI 540
QY      541 ANVYIAIVCNRRGFERADSEYTDKLQHTYSGHTPGMKIYIDPPTYBDPNEAVEFAKEI 600
      |||||||
Db      541 ANVYIAIVCNRRGFERADSEYTDKLQHTYSGHTPGMKIYIDPPTYBDPNEAVEFAKEI 600
QY      601 DISCVKLEQYIAGEFEVSGHKLTPGKREIFAITKISGTERKRRRPLSASTMGQ 660
      |||||||
Db      601 DISCVKLEQYIAGEFEVSGHKLTPGKREIFAITKISGTERKRRRPLSASTMGQ 660
QY      661 FDHPNVTHLEGVYTKSTPVMITTEFMENGLSDFLRONDQGFYIQLVGMRLGIAAGMKY 720
      |||||||
Db      661 FDHPNVTHLEGVYTKSTPVMITTEFMENGLSDFLRONDQGFYIQLVGMRLGIAAGMKY 720
QY      721 LADPNVYHRDLAARNILVNSNLCKVSDPGLSRPLEDDTSDPTYTSALGSKFPIRMTAPE 780
      |||||||
Db      721 LADPNVYHRDLAARNILVNSNLCKVSDPGLSRPLEDDTSDPTYTSALGSKFPIRMTAPE 780
QY      781 AIQYRKFTSASDVMSYGIWMMEVMSYGERPYMDTNDVYNATIEODYRLPPMDCPALH 840
      |||||||
Db      781 AIQYRKFTSASDVMSYGIWMMEVMSYGERPYMDTNDVYNATIEODYRLPPMDCPALH 840
QY      841 QLMIDCQKQRNRHPRKFGQIVNTLDMIRNPNLSIKAMAPLSSGINTPLDRTIPDYSFN 900
      |||||||
Db      841 QLMIDCQKQRNRHPRKFGQIVNTLDMIRNPNLSIKAMAPLSSGINTPLDRTIPDYSFN 900
QY      901 TVDEMLAIFMGQYKSEFANAAGTSPVVSOMMEDILRVGVLAGHOKILNSIOVMRA 960
      |||||||
Db      901 TVDEMLAIFMGQYKSEFANAAGTSPVVSOMMEDILRVGVLAGHOKILNSIOVMRA 960
QY      961 QMNOIOSVEV 970
      |||||||
Db      961 QMNOIOSVEV 970

```

RESULT 2
 148760
 protein-tyrosine kinase (EC 2.7.1.112) sek-3 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Feb-2000
 C:Accession: I48760; S42846
 R:Becker, N.; Seltanidou, T.; Murphy, P.; Mattei, M.G.; Topilko, P.; Nieto, M.A.; Wilkitt
 Mech. Dev. 47, 3-17, 1994
 A:Title: Several receptor tyrosine kinase genes of the Eph family are segmentally expres
 A:Reference number: I48759; MUID:95034306
 A:Accession: I48760
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-480 <RES>
 A:Cross-references: EMBL:X76011; NID:g460055; PIDN:CAAS3598.1; PID:g460056
 C:Genetics:
 A:Gene: Sek-3
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein k
 F:121-129/Domain: protein kinase ATP-binding motif
 F:404-470/Domain: SAM homology <SAM>

```

Query Match      30.5%; Score 296; DB 2; Length 480;
Best Local Similarity 99.7%; Pred. No. 1.4e-296;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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Db      84 TPQMKIYIDPPTYEDPNEAVEFAKEIDISCVKIEQYIAGEFEVSGHKLPGKREIF 143
QY      634 VAIKTKSGYTERKQRNDELSEASIMQFDHPNVIHLEGVYTKSTPVMITTEFMENGLSDS 693
      |||||||
Db      144 VAIKTKSGYTERKQRNDELSEASIMQFDHPNVIHLEGVYTKSTPVMITTEFMENGLSDS 203
QY      694 FLNONGQGFYIQLVGMRLGIAAGMKYLDPMNVYHRDLAARNILVNSNLCKVSDPGLSR 753
      |||||||
Db      204 FLNONGQGFYIQLVGMRLGIAAGMKYLDPMNVYHRDLAARNILVNSNLCKVSDPGLSR 263
QY      754 FLEDDTSDPTYTSALGSKFPIRMTAPEAIQYRKFTSASDVMSYGIWMMEVMSYGERPYMD 813
      |||||||
Db      264 FLEDDTSDPTYTSALGSKFPIRMTAPEAIQYRKFTSASDVMSYGIWMMEVMSYGERPYMD 323
QY      814 MFMQVYINAEQYELPLPPMDCPALHQLMIDCQKQRNRHPRKFGQIVNTLDMIRNPNLS 873
      |||||||
Db      324 MFMQVYINAEQYELPLPPMDCPALHQLMIDCQKQRNRHPRKFGQIVNTLDMIRNPNLS 383
QY      874 LKMAAPLSSGINTPLDRTIPDYSFNTEFNTDQWLEAIKMGQYKSEFANAAGTSPFDVVSOMM 933
      |||||||
Db      384 LKMAAPLSSGINTPLDRTIPDYSFNTEFNTDQWLEAIKMGQYKSEFANAAGTSPFDVVSOMM 933
QY      934 MEDILRVGVLAGHCKKILNSIOVMRAQMNQIOSVEV 970
      |||||||
Db      444 MEDILRVGVLAGHCKKILNSIOVMRAQMNQIOSVEV 480

```

```

RESULT 3
A57174
protein-tyrosine kinase (EC 2.7.1.112) erk - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Jun-2000
C:Accession: A57174; S23362; S40294; P00547
R:Salto, T.; Seki, N.; Matsuda, Y.; Kitahara, M.; Murata, M.; Kanda, N.; Nomura, N.;
Genomics 26, 382-384, 1995
A:Title: Identification of the human ERK gene as a putative receptor tyrosine kinase
A:Reference number: A57174; MUID:95324932
A:Accession: A57174
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-478 <SALT>
A:Cross-references: GB:D37827; NID:g1060894; PIDN:BA07073.1; PID:g1060895
R:Chan, J.; Watt, V.M.
Oncogene 6, 1057-1061, 1991
A:Title: erk and erk, new members of the eph subclass of receptor protein-tyrosine ki
A:Reference number: S23362; MUID:91296384
A:Accession: S23362
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 144-154, 'N', 156-204 <CHA>
A:Cross-references: EMBL:X59292
R:Watt, V.M.
submitted to the EMBL Data Library, May 1991
A:Reference number: S40294
A:Accession: S40294
A:Molecule type: mRNA
A:Residues: 144-204 <MAT>
A:Cross-references: EMBL:X59292; NID:g31222; PIDN:CA41981.1; PID:g31223
R:Iwase, T.; Tanaka, M.; Suzuki, M.; Naito, Y.; Sugimura, H.; Kino, T.
Biochem. Biophys. Res. Commun. 194, 698-705, 1993
A:Title: Identification of protein-tyrosine kinase genes preferentially expressed in
A:Reference number: P00547; MUID:93343925
A:Accession: P00547
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 132-162, 'N', 154-478, 'X' <IWA>
A:Cross-references: DDBJ:D14717
C:Genetics:  

A:Gene: GDB:ERK
A:Cross-references: GDB:128637; OMIM:176946
A:Map position: IP36.1-IP36.1
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein

```


Oncogene 10, 897-905, 1995
 A:Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein-ty
 A:Reference number: 158351; MUID:95206782
 A:Accession: 158351
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-998 <RES>
 A:Cross-references: GB:136642; NID:9551607; PIDN:AAA74243.1; PID:9551608
 C:Genetics:
 A:Gene: HEK11
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; transmembrane protein
 F:631-897/Domain: protein kinase homology <KIN>
 F:639-647/Region: protein kinase ATP-binding motif
 F:920-986/Domain: SAM homology <SAM>

Query Match 4.1%; Score 40; DB 2; Length 998;
 Best Local Similarity 100.0%; Pred. No. 3e-32;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 775 RMTAPEAIQYRKFTASADVSYGVMEVMSYGERPYDM 814
 DB 801 RMTAPEAIQYRKFTASADVSYGVMEVMSYGERPYDM 840

RESULT 8
 PT0187
 protein-tyrosine kinase (EC 2.7.1.112) tyro-5 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 04-Feb-2000
 C:Accession: PT0187
 R:Liati, C.; Lemke, G.
 Neuron 6, 691-704, 1991
 A:Title: An extended family of protein-tyrosine kinase genes differentially expressed in
 A:Reference number: PT0183; MUID:91222560
 A:Accession: PT0187
 A:Molecule type: mRNA
 A:Residues: 1-57 <LAI>
 A:Experimental source: sciatic nerve
 C:Genetics:
 A:Gene: tyro-5
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein k
 F:1-57/Domain: protein kinase homology (fragment) <KIN>

Query Match 3.8%; Score 37; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 3.1e-30;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 735 NIIVNSMLVCKVSDFGISRPLEDDTSDPYTSALGK 771
 DB 1 NIIVNSMLVCKVSDFGISRPLEDDTSDPYTSALGK 37

RESULT 9
 S33506
 protein-tyrosine kinase (EC 2.7.1.112) Cdk9 - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 04-Feb-2000
 C:Accession: S33506
 R:Sajjadi, F.G.; Pasquale, E.B.
 submitted to the EMBL data library, December 1992
 A:Description: Five additional avian Eph-related tyrosine kinases are differentially exp
 A:Reference number: S33502
 A:Accession: S33506
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-612 <SAJ>
 A:Cross-references: EMBL:219060
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein k

F:63-147/Domain: fibronectin type III repeat homology <3FR>
 F:245-513/Domain: protein kinase homology <KIN>
 F:253-261/Region: protein kinase ATP-binding motif
 F:536-602/Domain: SAM homology <SAM>

Query Match 3.7%; Score 36; DB 2; Length 612;
 Best Local Similarity 100.0%; Pred. No. 2.6e-28;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 723 DMNVHRDLAARNILVNSMLVCKVSDFGISRPLEDD 758
 DB 365 DMNVHRDLAARNILVNSMLVCKVSDFGISRPLEDD 400

RESULT 10
 I48761
 protein-tyrosine kinase (EC 2.7.1.112) sek-4 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Feb-2000
 C:Accession: I48761; S42847
 R:Becker, N.; Seltanidou, T.; Murphy, P.; Mattei, M.G.; Topilko, P.; Nieto, M.A.; Wll
 Mech. Dev. 47, 3-17, 1994
 A:Title: Several receptor tyrosine kinase genes of the Eph family are segmentally exp
 A:Reference number: I48759; MUID:95034306
 A:Accession: I48761
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-275 <BEC>
 A:Cross-references: EMBL:X76012; NID:9460057; PIDN:CA53599.1; PID:9460058
 C:Genetics:
 A:Gene: sek-4
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein
 F:1-176/Domain: protein kinase homology (fragment) <KIN>
 F:199-265/Domain: SAM homology <SAM>

Query Match 3.6%; Score 35; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 1.4e-27;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 MNVHRDLAARNILVNSMLVCKVSDFGISRPLEDD 758
 DB 29 MNVHRDLAARNILVNSMLVCKVSDFGISRPLEDD 63

RESULT 11
 I49071
 protein kinase - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
 C:Accession: I49071
 R:Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
 Mech. Dev. 48, 153-164, 1994
 A:Title: Identification of novel protein kinases expressed in the myocardium of the d
 A:Reference number: I49071; MUID:95200798
 A:Accession: I49071
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-938 <RES>
 A:Cross-references: EMBL:U11493; NID:9595418; PIDN:AAA67925.1; PID:9595419
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
 C:Keywords: ATP; transmembrane protein
 F:571-839/Domain: protein kinase homology <KIN>
 F:579-587/Region: protein kinase ATP-binding motif
 F:862-928/Domain: SAM homology <SAM>

Query Match 3.6%; Score 35; DB 2; Length 938;
 Best Local Similarity 100.0%; Pred. No. 4.1e-27;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 758
 DB 692 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 726

RESULT 12

150611
 protein-tyrosine kinase (EC 2.7.1.112) Cdk10 - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Feb-2000
 C:Accession: 150611; S33502
 R:Sajjadi, F.G.; Pasquale, E.B.
 Oncogene 8, 1807-1813, 1993
 A:Title: Five novel avian Eph-related tyrosine kinases are differentially expressed.
 A:Reference number: 150611; MUID:93288394
 A:Accession: 150611
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-988 <SAS>
 A:Cross-references: EMBL:Z19061; NID:g312201; PIDN:CAA79511.1; PID:g312202
 C:Genetics:
 A:Gene: Cdk10
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein K1
 F:621-889/Domain: protein kinase homology <KIN>
 F:629-637/Region: protein kinase ATP-binding motif
 F:912-978/Domain: SAM homology <SAM>

Query Match 3.6%; Score 35; DB 2; Length 988;
 Best Local Similarity 100.0%; Pred. No. 4.3e-27;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 758
 DB 742 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 776

RESULT 13

148653
 mouse developmental kinase 5 (MDK5) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
 C:Accession: 148653
 R:Ciossek, T.; Ierch, M.M.; Ullrich, A.
 Oncogene 11, 2085-2095, 1995
 A:Title: Cloning, characterization, and differential expression of MDK2 and MDK5, two novel mouse tyrosine kinases.
 A:Reference number: 148652; MUID:96074837
 A:Accession: 148653
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-993 <RES>
 A:Cross-references: EMBL:Z49086; NID:g1089899; PIDN:CAA86910.1; PID:g1089900
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; transmembrane protein
 F:626-894/Domain: protein kinase homology <KIN>
 F:634-642/Region: protein kinase ATP-binding motif
 F:917-983/Domain: SAM homology <SAM>

Query Match 3.6%; Score 35; DB 2; Length 993;
 Best Local Similarity 100.0%; Pred. No. 4.3e-27;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 758
 DB 747 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 781

RESULT 14

S37627
 protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human
 C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 03-Aug-1995 #text_change 04-Feb-2000
 C:Accession: S37627
 R:Bohme, B.; Holtrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Streibhardt, K.; Ru
 Oncogene 8, 2857-2862, 1993
 A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.
 A:Reference number: S37627; MUID:93390963
 A:Accession: S37627
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-998 <BOE>

A:Cross-references: EMBL:X75208; NID:g406867; PIDN:CAA53021.1; PID:g406868
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein
 F:631-899/Domain: protein kinase homology <KIN>
 F:639-647/Region: protein kinase ATP-binding motif
 F:922-988/Domain: SAM homology <SAM>

Query Match 3.6%; Score 35; DB 2; Length 998;
 Best Local Similarity 100.0%; Pred. No. 4.3e-27;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 758
 DB 752 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 786

RESULT 15

150612
 protein-tyrosine kinase (EC 2.7.1.112) Cdk6 - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Feb-2000
 C:Accession: 150612; S33503
 R:Sajjadi, F.G.; Pasquale, E.B.
 Oncogene 8, 1807-1813, 1993
 A:Title: Five novel avian Eph-related tyrosine kinases are differentially expressed.
 A:Reference number: 150611; MUID:93288394
 A:Accession: 150612
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-952 <SAS>
 A:Cross-references: EMBL:Z19110; NID:g312901; PIDN:CAA79526.1; PID:g312902
 C:Genetics:
 A:Gene: Cdk6
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein
 F:585-853/Domain: protein kinase homology <KIN>
 F:593-601/Region: protein kinase ATP-binding motif
 F:876-942/Domain: SAM homology <SAM>

Query Match 3.3%; Score 32; DB 2; Length 952;
 Best Local Similarity 100.0%; Pred. No. 5.2e-24;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 691 LDSFLRNDGQFTVIQVLGMLRGIAAGMKYLA 722
 DB 673 LDSFLRNDGQFTVIQVLGMLRGIAAGMKYLA 704

Search completed: July 24, 2001, 16:33:51
 Job time: 137 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:33:29 ; Search time 14.77 Seconds

(without alignments)
2249.683 Million cell updates/sec

Title: US-09-378-759-11

Perfect score: 970
Sequence: 1 LIAAVEETLMOSTTAFELG.....IINSTQVRAQMNQISVEV 970

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	57.4	1055	EPB2_HUMAN	P29323 homo sapien
2	322	33.2	993	EPB2_MOUSE	P54756 mus musculu
3	103	10.6	987	EPB2_COTJA	Q90344 coturnix co
4	103	10.6	1004	EPB2_CHICK	P28693 gallus gall
5	40	4.1	993	EPB7_CHICK	O42422 gallus gall
6	40	4.1	998	EPB7_HUMAN	O45375 homo sapien
7	40	4.1	998	EPB7_MOUSE	O61772 mus musculu
8	40	4.1	998	EPB7_RAT	P54759 rattus norv
9	36	3.7	1002	EPB5_CHICK	O07457 gallus gall
10	35	3.6	988	EPB3_CHICK	O07458 gallus gall
11	35	3.6	993	EPB3_MOUSE	P54754 mus musculu
12	35	3.6	998	EPB3_HUMAN	P54753 homo sapien
13	33	3.4	974	EPB3_XENLA	O91735 xenopus lae
14	32	3.3	984	EPB1_CHICK	O07454 gallus gall
15	32	3.3	984	EPB1_HUMAN	P54752 homo sapien
16	31	3.2	992	EPB4_BRARE	O31318 brachydanio
17	31	3.2	902	EPB8_XENLA	O31736 xenopus lae
18	31	3.2	984	EPB1_RAT	P09759 rattus norv
19	31	3.2	985	EPB8_XENLA	O91694 xenopus lae
20	31	3.2	985	EPB8_XENLA	O91571 xenopus lae
21	31	3.2	986	EPB4_XENLA	O31845 xenopus lae
22	31	3.2	986	EPB4_CHICK	O07456 gallus gall
23	31	3.2	986	EPB4_HUMAN	P54764 homo sapien
24	31	3.2	986	EPB4_MOUSE	O03137 mus musculu
25	31	3.2	987	EPB4_HUMAN	P54760 homo sapien
26	31	3.2	987	EPB4_MOUSE	P54761 mus musculu
27	30	3.1	976	EPB2_HUMAN	P29337 homo sapien
28	30	3.1	977	EPB2_MOUSE	O03145 mus musculu
29	28	2.9	948	EPB6_RAT	P54758 rattus norv
30	28	2.9	1013	EPB5_CHICK	P54755 gallus gall
31	26	2.9	1035	EPB6_MOUSE	O62413 mus musculu
32	26	2.7	500	EPB3_BRARE	O31317 brachydanio
33	24	2.5	877	EPB5_MOUSE	O60629 mus musculu

ALIGNMENTS

RESULT	1	STANDARD	PRT	1055 AA.	
EPB2_HUMAN					
ID	EPB2_HUMAN				
AC	P29323; O43477;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-OCT-2000 (Rel. 40, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	EPHRAIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EPH-3) (DRT) (RECEPTOR PROTEIN-TYROSINE KINASE HEK5) (BRK).				
GN	EPHB2 OR EPHB3 OR ERK OR DRT OR HEK5.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=96154673; PubMed=8598679;				
RA	Itegaki N., Tang X.X., Lin X.-G., Biegel J.A., Allen C.,				
RT	"Molecular characterization and chromosomal localization of DRT (EPH3): a developmentally regulated human protein-tyrosine kinase gene of the EPH family.";				
RT	Hum. Mol. Genet. 4:2033-2045(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).				
RC	TISSUE=Gastric carcinoma;				
RX	MEDLINE=93343925; PubMed=7688222;				
RA	Iwase T., Tanaka M., Suzuki M., Naito Y., Sugimura H., Kino I.,				
RT	"Identification of protein-tyrosine kinase genes preferentially expressed in embryo stomach and gastric cancer.";				
RT	Biochem. Biophys. Res. Commun. 194:698-705(1993).				
RN	[3]				
RP	SEQUENCE FROM N.A. (LONG ISOFORM).				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=98359217; PubMed=9696046;				
RA	Tang X.X., Pleasure D.E., Brodeur G.M., Itegaki N.,				
RT	"A variant transcript encoding an isoform of the human protein tyrosine kinase EPHB2 is generated by alternative splicing and alternative use of polyadenylation signals.";				
RT	Oncogene 17:521-526(1998).				
RN	[4]				
RP	SEQUENCE OF 15-986 FROM N.A. (SHORT ISOFORM).				
RC	TISSUE=Brain;				
RX	MEDLINE=95206782; PubMed=7898931;				
RA	Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,				
RT	Basu R., Weicher A.A.;				
RT	"cDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine kinases.";				
RT	Oncogene 10:897-905(1995).				
RN	[5]				
RP	SEQUENCE OF 509-986 FROM N.A. (SHORT ISOFORM).				
RC	TISSUE=Brain;				
RA	Saito T., Nishihiko S., Kishihara M., Murata M., Yamamoto Y.,				
RA	Hori T., Matsuda Y.;				

RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 652-712 FROM N.A.
RX MEDLINE-91296384; PubMed-1648701;
RA Chan J., Walt V.M.;
RT "eek and erk, new members of the eph subclass of receptor protein-
tyrosine kinases.";
RL Oncogene 6:1057-1061(1991).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 910-986 (SHORT ISOFORM).
RA MEDLINE-99132419; PubMed-9933164;
RA Thamos C.D., Goodwill K.E., Bowie J.U.;
RT "Oligomeric structure of the human EphB2 receptor SAM domain.";
RL Science 283:833-836(1999).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. THE LIGAND-
ACTIVATED FORM INTERACTS WITH MULTIPLE PROTEINS, INCLUDING GTPASE-
ACTIVATING PROTEIN (RASGAP) THROUGH ITS SH2 DOMAIN. RASGAP BINDS
EPH2 THROUGH THE JUXTAMEMBRANE TYROSINES RESIDUES (BY
SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM/EPHB2V (SHOWN HERE)
AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: BRAIN, HEART, LUNG, KIDNEY, PLACENTA,
PANCREAS, LIVER AND SKELETAL MUSCLE. PREFERENTIALLY EXPRESSED IN
FETAL BRAIN.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
RECEPTOR SUBFAMILY.
CC -----
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DR EMBL: L41939; AAA99310.1; -
DR EMBL: D31661; BAA06306.1; -
DR EMBL: AF025304; AAB94602.1; -
DR EMBL: D14717; BAA03537.1; -
DR EMBL: L36643; AAA74244.1; -
DR EMBL: D37827; BAA7073.1; -
DR EMBL: X59292; CAA1981.1; -
DR PDB: 1BAF; 16-FEB-99.
DR MIM: 600997; -
DR InterPro: IPR000561; -
DR InterPro: IPR000719; -
DR InterPro: IPR001090; -
DR InterPro: IPR001245; -
DR InterPro: IPR001426; -
DR InterPro: IPR001660; -
DR InterPro: IPR001777; -
DR Pfam: PF01404; EPH_Lbd; 1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; kinase; 1.
DR PRINTS: PR00014; ENYPEPIL1.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR Transfaser: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure;
KW Alternative splicing; Repeat.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1055 EPHRIN TYPE-B RECEPTOR 2.

FT	DOMAIN	19	543	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	544	564	POTENTIAL.
FT	DOMAIN	565	1055	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	184	324	CYS-RICH.
FT	DOMAIN	325	418	FIBRONECTIN TYPE-III.
FT	DOMAIN	436	520	FIBRONECTIN TYPE-III.
FT	DOMAIN	621	884	PROTEIN KINASE.
FT	DOMAIN	911	986	SAM.
FT	SITE	984	986	PDZ-BINDING MOTIF (POTENTIAL) (IN SHORT ISOFORM).
FT	NP_BIND	627	635	ATP (BY SIMILARITY).
FT	ACT_SITE	653	653	ATP (BY SIMILARITY).
FT	MOD_RES	746	746	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD_RES	596	596	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD_RES	602	602	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD_RES	780	780	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES	930	930	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	CARBOHYD	265	265	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	336	336	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	428	428	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	482	482	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	986	986	G -> V (IN SHORT ISOFORM).
FT	VARIANT	987	1055	MISSING (IN SHORT ISOFORM).
FT	CONFLICT	671	671	A -> R.
FT	CONFLICT	1	20	/FTID-VAR 004162.
FT	CONFLICT	154	154	MALRRGALLPLLAANE -> MVVPLALPVCTYA (IN REF. 2).
FT	CONFLICT	476	476	G -> D (IN REF. 2).
FT	CONFLICT	532	532	K -> KQ (IN REF. 2).
FT	CONFLICT	495	496	E -> D (IN REF. 2).
FT	CONFLICT	568	568	MISSING (IN REF. 4).
FT	CONFLICT	589	589	R -> RR (IN REF. 1).
FT	CONFLICT	788	788	M -> I (IN REF. 4).
FT	CONFLICT	833	833	I -> F (IN REF. 4).
FT	CONFLICT	923	923	S -> A (IN REF. 2 AND 5).
FT	CONFLICT	956	956	E -> K (IN REF. 2 AND 5).
FT	CONFLICT	958	558	L -> V (IN REF. 3).
FT	CONFLICT	958	558	V -> L (IN REF. 1).
SO	SEQUENCE	1055 AA; 117506 MW; D0AA2C8CEBECDB88 CRC64;		

Query Match 57.4%; Score 557; DB 1; Length 1055;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 937; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
QY 1 LLAAYETLMDSTYFAELGMMVHPRSSGMEVSGYBNNMTIRTYGVAVPSSQNNMLR 60
DB 15 LLAAYETLMDSTYFAELGMMVHPRSSGMEVSGYBNNMTIRTYGVAVPSSQNNMLR 74
QY 61 TKFIRRGAAHRIHVEKFSVRCSSIPSPGSKETFNLYYEADPDSATKTFPNMEMP 120
DB 75 TKFIRRGAAHRIHVEKFSVRCSSIPSPGSKETFNLYYEADPDSATKTFPNMEMP 134
QY 121 WKVDTIAADESESCVDLGGRYMKINTEVRSFGVRSRSGFYLAFODYGGCMLSIAVRVEY 180
DB 135 WKVDTIAADESESCVDLGGRYMKINTEVRSFGVRSRSGFYLAFODYGGCMLSIAVRVEY 194
QY 181 RRCPRITONGALFOETLSAESTSYAARGSCIANEEDVDPKILYCNDDGEMVPIGRC 240
DB 195 RRCPRITONGALFOETLSAESTSYAARGSCIANEEDVDPKILYCNDDGEMVPIGRC 254
QY 241 MCKAGEAVENTGVCNGCSGTFKANOGDEACTHCPINSRTSEGTANCVRNGYRADL 300
DB 255 MCKAGEAVENTGVCNGCSGTFKANOGDEACTHCPINSRTSEGTANCVRNGYRADL 314
QY 301 DPLDMCCTTIPAPCAVVISVNETSLMEWTPPRDSGREDLVYNIICKSCSGRGACTR 360
DB 315 DPLDMCCTTIPAPCAVVISVNETSLMEWTPPRDSGREDLVYNIICKSCSGRGACTR 374
QY 361 GCDNVOYAROGLEHPRITISDLAHQYTFEIQAVNVTVTQSPSPQFASVNTITNQA 420
DB 375 GCDNVOYAROGLEHPRITISDLAHQYTFEIQAVNVTVTQSPSPQFASVNTITNQA 434

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OY 421 APSAVSIMHOVSRVSTISLSQOPDQNGVILDELOYEKEKLSXNATAIKSPNTVT 480
DB 435 APSVASTIMHOVSRVSTISLSQOPDQNGVILDELOYEKEKLSXNATAIKSPNTVT 494
OY 481 --GLKAGAIYFQVRAVAGYRGYSGKMFQMTAEAVOTSIOEKLPLIGSSAGLVF 538
DB 495 VQGLKAGAIYFQVRAVAGYRGYSGKMFQMTAEAVOTSIOEKLPLIGSSAGLVF 554
OY 539 LIAVVAIAVCNRRGFERADSEYTKLOHYTSGHITPGMKIYIDPPTYEDPPNVAVERFAK 598
DB 555 LIAVVAIAVCNRRGFERADSEYTKLOHYTSGHITPGMKIYIDPPTYEDPPNVAVERFAK 614
OY 599 EIDISCVKIEOVGAGEFEVCGHKLKQKREIFAIVATTLKSGYTERKORPFLSEASIM 658
DB 615 EIDISCVKIEOVGAGEFEVCGHKLKQKREIFAIVATTLKSGYTERKORPFLSEASIM 674
OY 659 GQDPHNVITHLEGVTKSTPVMTITFEFMENGLSDFLRNDQOFYIOVLGMLRGIAQM 718
DB 675 GQDPHNVITHLEGVTKSTPVMTITFEFMENGLSDFLRNDQOFYIOVLGMLRGIAQM 734
OY 719 KYIADNMYHRLAARNILVNSNLCKVSDFGLSREFLEDSDPTVTSALGKFPIRMWA 778
DB 735 KYIADNMYHRLAARNILVNSNLCKVSDFGLSREFLEDSDPTVTSALGKFPIRMWA 794
OY 779 PEAIQYRKFTSASDVMSYGIWMEVMSYGERPYMTNDVINAIEDYRLRPPMDCPSA 838
DB 795 PEAIQYRKFTSASDVMSYGIWMEVMSYGERPYMTNDVINAIEDYRLRPPMDCPSA 854
OY 839 LIQMLDMCQKDRNHRPKRGQIVNTLDMKIRNPSLKAAPLSSGINSPLDRTTPDYS 898
DB 855 LIQMLDMCQKDRNHRPKRGQIVNTLDMKIRNPSLKAAPLSSGINSPLDRTTPDYS 914
OY 899 FMTVDEMLEATIMGOYKESFANAAGTSPDVYSQMMEDILR 939
DB 915 FMTVDEMLEATIMGOYKESFANAAGTSPDVYSQMMEDILR 955

RESULT 2
EPH2_MOUSE STANDARD: PRT: 993 AA.
ID AC P54763.062213:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EPH-3) (NRK) (SEK-3) (FRAGMENT).
GN EPHB2 OR EPH3 OR NRK OR SEK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN 11
RP SEQUENCE FROM N.A.
RA Henkemeyer M.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE OF 515-993 FROM N.A.
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE=95034306; PubMed=7947319;
RA Becker N., Settenidou T., Murphy P., Mattel M.-G., Topilko P.,
RA Nieto A., Wilkinson D.G., Charney P., Gilardi P.;
RT "Several receptor tyrosine kinase genes of the Eph family are
RT segmentally expressed in the developing hindbrain.";
RL Mech. Dev. 47:3-17(1994).
RN 13
RP FUNCTION.
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wldeman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors
RT in the mouse spinal cord: a possible role in constraining the
RT orientation of longitudinally projecting axons.";
RL Development 127:1397-1410(2000)
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. CAN

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CC CC FUNCTION IN ASPECTS OF RETINAL GANGLION CELL AXON GUIDANCE TO THE
CC CC OPTIC DISK EVEN LACKING ITS TYROSINE KINASE DOMAIN. THE LIGAND-
CC CC ACTIVATING FORM INTERACTS WITH MULTIPLE PROTEINS, INCLUDING GTPASE-
CC CC ACTIVATING PROTEIN (RASGAP) THROUGH ITS SH2 DOMAIN. RASGAP BINDS
CC CC EPHB2 THROUGH THE JUXTAMEMBRANE TYROSINES RESIDUES (BY
CC CC SIMILARITY).
CC CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC CC PROTEIN TYROSINE PHOSPHATE.
CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -1- TISSUE SPECIFICITY: EXPRESSED IN CELLS OF THE DEVELOPING OUTER
CC CC RETINA.
CC CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC CC RECEPTOR SUBFAMILY.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: L25890; AAA72411.1; ALT_INIT.
CC CC DR EMBL: X76011; CA53598.1; -.
CC CC DR HSSP: P00523; 2PTK
CC CC DR MGD: MGI:99611; Ephb2.
CC CC DR InterPro: IPR000561; -.
CC CC DR InterPro: IPR000719; -.
CC CC DR InterPro: IPR001090; -.
CC CC DR InterPro: IPR001245; -.
CC CC DR InterPro: IPR001428; -.
CC CC DR InterPro: IPR001660; -.
CC CC DR InterPro: IPR001777; -.
CC CC DR Pfam: PF01404; Eph_1bd; 1.
CC CC DR Pfam: PF00536; SAM; 1.
CC CC DR Pfam: PF00041; fn3; 2.
CC CC DR Pfam: PF00069; pkinase; 1.
CC CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC CC DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
CC CC DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
CC CC DR PROSITE: PS01186; EGF_2; UNKNOWN; 1.
CC CC KM Transferase: Tyrosine-protein kinase.
CC CC KM Receptor: Transmembrane; Glycoprotein; Signal; Repeat.
CC CC FT NON_TER 1 1
CC CC FT SIGNAL <1 25
CC CC FT CHAIN 26 993
CC CC FT DOMAIN 26 550
CC CC FT TRANSMEM 571
CC CC FT DOMAIN 572 993
CC CC FT DOMAIN 191 328
CC CC FT DOMAIN 329 438
CC CC FT DOMAIN 439 536
CC CC FT DOMAIN 628 891
CC CC FT SITE 918 993
CC CC FT NP_BIND 634 642
CC CC FT BINDING 660 660
CC CC FT ACT_SITE 753 753
CC CC FT MOD_RES 603 603
CC CC FT MOD_RES 609 609
CC CC FT MOD_RES 787 787
CC CC FT MOD_RES 937 937
CC CC FT CARBOHYD 272 272
CC CC FT CARBOHYD 343 343
CC CC FT CARBOHYD 435 435
CC CC FT CARBOHYD 489 489
CC CC FT CONFLICT 575 575
CC CC SEQUENCE 993 AA; 110628 MW; A0E1A695F46587E8 CRC64;

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OX NCBI_TaxID=9031:
 RN (1)
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RC TISSUE-Embryo;
 RX MEDLINE=92144672; PubMed=1664238;
 RA Pasquale E.B.;
 RT "identification of chicken embryo kinase 5, a developmentally regulated receptor-type tyrosine kinase of the Eph family.";
 RL Cell Regul. 2:523-534(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RC TISSUE-Brain;
 RX MEDLINE=93288394; PubMed=8510926;
 RA Sejjadi F.G., Pasquale E.B.;
 RT "Five novel avian Eph-related tyrosine kinases are differentially expressed.";
 RL Oncogene 8:1807-1813(1993).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. PROBABLY AN IMPORTANT COMPONENT OF SIGNAL TRANSDUCTION PATHWAYS.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM/CEK5+ (SHOWN HERE) AND A SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION THROUGHOUT DEVELOPMENT AND SUSTAINED EXPRESSION IN ADULT BRAIN. THE LONGER FORM (CEK5+) IS SPECIFICALLY EXPRESSED IN THE CENTRAL NERVOUS SYSTEM.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.
 CC -----
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 CC -----
 CC HSSP; M62325; AAA48667.1; ALT_INIT.
 DR HSSP; P00523; 2PTR.
 DR Interpro: IPR000561; -
 DR Interpro: IPR000719; -
 DR Interpro: IPR001090; -
 DR Interpro: IPR001245; -
 DR Interpro: IPR001426; -
 DR Interpro: IPR001660; -
 DR Interpro: IPR001777; -
 DR Pfam: PF001404; Eph_Ibd; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PRO0014; FNTYPEIIT.
 DR PRINTS: PRO0109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR Transfaser: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
 KW Repeat.
 FT STGNL; 1 19
 FT CHAIN; 20 1004
 FT DOMAIN; 545 565
 FT TRANSMEM; 545 565
 FT DOMAIN; 566 1004
 FT DOMAIN; 20 321
 FT DOMAIN; 326 419
 FT DOMAIN; 437 521
 FT DOMAIN; 437 521

FT DOMAIN 639 902
 FT DOMAIN 929 1004
 FT SITE 1002 1004
 FT NE_BIND 645 653
 FT BINDING 671 671
 FT ACT_SITE 764 764
 FT MOD_RES 614 614
 FT MOD_RES 620 620
 FT MOD_RES 798 798
 FT MOD_RES 948 948
 FT CARBOHYD 266 266
 FT CARBOHYD 337 337
 FT CARBOHYD 429 429
 FT CARBOHYD 478 478
 FT CARBOHYD 483 483
 FT VARSPPLIC 591 606
 SQ SEQUENCE 1004 AA; 111963 MW; 8D26213970ECC6E0 CRC64;
 Query Match 10.6%; Score 103; DB 1; Length 1004;
 Best local Similarity 100.0%; Pred. No. 1.2e-102;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 574 TPQMKIYIDPFTYEDPNEAVREFAKEDISCVNIEGVIGAGEGEVCSGLKLPKREIF 633
 DB 608 TPQMKIYIDPFTYEDPNEAVREFAKEDISCVNIEGVIGAGEGEVCSGLKLPKREIF 667
 OY 634 VAIKTLKSGTEKORDPFLSEASIMGOFDPNVIHLEGVTVS 676
 DB 668 VAIKTLKSGTEKORDPFLSEASIMGOFDPNVIHLEGVTVS 710
 RESULT 5
 EPAY CHICK STANDARD; PRT; 993 AA.
 AC 042422;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (BC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEPHA7) (TYROSINE-PROTEIN KINASE RECEPTOR CEK11).
 GN CEPHA7 OR CEK11.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Embryo;
 RX MEDLINE=98092111; PubMed=9431814;
 RA Araujo M., Nieto M.A.;
 RT "The expression of chick EphA7 during segmentation of the central and peripheral nervous system.";
 RL Mech. Dev. 68:173-177(1997).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN FAMILY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM.
 CC RESTRICTED TO PHOSOMERES 1 AND 2 IN THE Drosophila AND ALL THE HOMOMERES IN THE HINDRAIN DURING SEGMENTATION STAGES. LATER ON, A SUPERIMPOSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION OF SEVERAL AXONAL TRACTS. IN THE SOMITIC MESODERM, THE EXPRESSION CORRELATES WITH SEGMENTATION AND THE GUIDANCE OF BOTH NEURAL CREST AND MOTOR AXONS THROUGH THE SCIOTOMES.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.
 CC -----
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EMBL: Y14271; CAA74643.1; -
HSP: P00523; 2PTK.
InterPro: IPR000719; -
InterPro: IPR001090; -
InterPro: IPR001245; -
InterPro: IPR001426; -
InterPro: IPR001660; -
InterPro: IPR001777; -
Pfam: PF01404; EPH_1bd; 1.
Pfam: PF00536; SAM; 1.
Pfam: PF00041; fn3; 2.
Pfam: PF00069; pkinaase; 1.
PRINTS: PR00014; FNTYPEIII.
PRINTS: PR00107; TYRKINASE.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS00119; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE: PS01186; EGF_2; UNKNOWN_1.
Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 30
FT CHAIN 31 993
FT DOMAIN 31 551
FT TRANSMEM 552 572
FT DOMAIN 573 993
FT DOMAIN 192 328
FT DOMAIN 329 438
FT DOMAIN 439 536
FT DOMAIN 628 889
FT DOMAIN 916 993
FT SITE 991 993
FT NP_BIND 991 634
FT DISULFID 74 109
FT BINDING 660 660
FT ACT_SITE 753 753
FT MOD_RES 603 603
FT MOD_RES 609 609
FT MOD_RES 786 786
FT MOD_RES 935 935
FT CARBOHYD 343 343
FT CARBOHYD 410 410
SEQUENCE 993 AA; 11366 MW; EECF9603047606BD CRC64;

Query Match 4.18; Score 40; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 1.9e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 775 RMTAPEAIQYRKFTSADVMSYGVMEVMSYGERPMD 814
Db 796 RMTAPEAIQYRKFTSADVMSYGVMEVMSYGERPMD 835

RESULT 6
EPA7_HUMAN STANDARD; PRT; 998 AA.
AC Q15375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EHK-3) (EPH HOMOLOG KINASE-3) (RECEPTOR PROTEIN-
DE TYROSINE KINASE HEK1).
GN EPHAY OR EHK3 OR HEK1.
OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95206782; PubMed=7898931;
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA Basu R., Welcher A.A.;
RT "cDNA cloning and tissue distribution of five human EPH-like receptor
protein-tyrosine kinases";
RL Oncogene 10:897-905(1995).
CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).

EMBL: L36642; AAA74243.1; -
HSP: P00523; 2PTK.
MIM: 602190; -
InterPro: IPR000561; -
InterPro: IPR000719; -
InterPro: IPR001090; -
InterPro: IPR001245; -
InterPro: IPR001426; -
InterPro: IPR001660; -
InterPro: IPR001777; -
Pfam: PF01404; EPH_1bd; 1.
Pfam: PF00536; SAM; 1.
Pfam: PF00041; fn3; 2.
Pfam: PF00069; pkinaase; 1.
PRINTS: PR00014; FNTYPEIII.
PRINTS: PR00107; TYRKINASE.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS00119; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE: PS01186; EGF_2; UNKNOWN_1.
Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 998
FT DOMAIN 25 556
FT TRANSMEM 557 572
FT DOMAIN 578 998
FT DOMAIN 192 328
FT DOMAIN 329 438
FT DOMAIN 439 536
FT DOMAIN 633 894
FT DOMAIN 921 998
FT SITE 996 998
FT NP_BIND 996 639
FT BINDING 663 647
FT ACT_SITE 665 665
FT ACT_SITE 758 758
FT MOD_RES 608 608
FT MOD_RES 614 614
FT MOD_RES 791 791
FT MOD_RES 940 940

FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 998 AA; 112096 MW; 479B9CA0D2B06EB CRC64;
 Query Match 4.18; Score 40; DB 1; Length 998;
 Best Local Similarity 100.0%; Pred. No. 1,9e-34;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 775 RWTAPFAIOTRKFTSASDVMSYGIWMVMSYGERPYWDM 814
 Db 801 RWTAPFAIOTRKFTSASDVMSYGIWMVMSYGERPYWDM 840
 RESULT 7
 EPAT_MOUSE STANDARD; PRT; 998 AA.
 AC 061772; 061773; 061774; 061505;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR EHK-3) (EPH HOMOLOG KINASE-3) (EMBRYONIC BRAIN
 DE KINASE) (EBK) (DEVELOPMENTAL KINASE 1) (MDK-1).
 GN EPHA7 OR EHK3 OR EBK OR MDK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RA MEDLINE=95124729; PubMed=7824284;
 RA Ciosek T., Millauer B., Ullrich A.;
 RT "Identification of alternatively spliced mRNAs encoding variants of
 RT MDK1, a novel receptor tyrosine kinase expressed in the murine
 RT nervous system.";
 RT Oncogene 10:97-108(1995).
 RL [2]
 RP SEQUENCE OF 431-998 FROM N.A. (ISOFORM MDK1).
 RC TISSUE-Brain;
 RA MEDLINE=96081374; PubMed=8541219;
 RA Ellis J., Liu Q., Breitman M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling H.,
 RA Fletcher F.A., Ziegler S.F., Rogers J.H.;
 RT "Embryo brain kinase: a novel gene of the eph/ek receptor tyrosine
 RT kinase family.";
 RT Mech Dev. 52:319-341(1995).
 RL [1]
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: MDK1 (SHOWN HERE), MDK1-1, MDK1-
 CC 2, MDK1-T1 AND MDK1-T2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN EMBRYO, IN ADULT,
 CC EXPRESSION RESTRICTED TO HIPPOCAMPUS, TESTIS AND SPLEEN.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X79082; CAAS5687.1; -;
 DR EMBL; X79083; CAAS5688.1; -;
 DR EMBL; X79084; CAAS5689.1; -;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DR EMBL; X81466; CAAS7224.1; -;
 DR HSSP; P00523; 2PTR.
 DR MGD; MG1:95276; EphA7.
 DR InterPro: IPR000561;
 DR InterPro: IPR000739;
 DR InterPro: IPR001090;
 DR InterPro: IPR001245;
 DR InterPro: IPR001426;
 DR InterPro: IPR001660;
 DR InterPro: IPR001777;
 DR Pfam: PF01404; Eph_1bd; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; kinase; 1.
 DR PRINTS; PR00014; FNTYPEIIT.
 DR PRINTS; PR00109; TYRKINASE.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN; 1.
 KW transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing.
 FT SIGNAL 1 29
 FT CHAIN 30 998
 FT DOMAIN 30 556
 FT TRANSMEM 557 577
 FT DOMAIN 578 998
 FT DOMAIN 192 328
 FT DOMAIN 329 438
 FT DOMAIN 439 536
 FT DOMAIN 633 894
 FT DOMAIN 921 998
 FT SITE 996 998
 FT NF_BIND 639 647
 FT BINDING 665 665
 FT ACT_SITE 758 758
 FT MOD_RES 608 608
 FT MOD_RES 614 614
 FT MOD_RES 791 791
 FT MOD_RES 940 940
 FT CARBOHYD 343 343
 FT CARBOHYD 410 410
 FT CARBOHYD 410 544
 FT VARSPPLIC 601 604
 FT VARSPPLIC 601 610
 FT VARSPPLIC 611 998
 FT VARSPPLIC 600 626
 FT VARSPPLIC 627 998
 FT CONFLICT 480 480
 SQ SEQUENCE 998 AA; 11874 MW; 81C553BE15AE2FA CRC64;
 Query Match 4.18; Score 40; DB 1; Length 998;
 Best Local Similarity 100.0%; Pred. No. 1,9e-34;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 775 RWTAPFAIOTRKFTSASDVMSYGIWMVMSYGERPYWDM 814
 Db 801 RWTAPFAIOTRKFTSASDVMSYGIWMVMSYGERPYWDM 840
 RESULT 8
 EPAT_MOUSE STANDARD; PRT; 998 AA.
 ID EPAT_MOUSE
 AC P54759;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 KINASE RECEPTOR EHK-3) (EPH HOMOLOG KINASE-3).
 GN EPHA7 OR EHK3 OR EHK-3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP MEDLINE-95249272; PubMed-7731712;
 RX Valenzuela D.M., Rojas E., Griffiths J.A., Compton D.L., Gisser M.,
 RA Ip N.Y., Goldfarb M., Yancopoulos G.D.;
 RT "Identification of full-length and truncated forms of Ehk-3, a novel
 member of the Eph receptor tyrosine kinase family.";
 RL Oncogene 10:1573-1580(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC TRUNCATED ISOFORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE
 CC TRUNCATED FORM LACKS THE KINASE DOMAIN. THE LONG FORM IS MORE
 CC WIDELY EXPRESSED IN THE EMBRYO.
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U21954; AAA86830.1; -
 DR EMBL: U21955; AAA86831.1; -
 DR HSSP: P00523; 2PTK.
 DR InterPro: IPR000561; -
 DR InterPro: IPR000719; -
 DR InterPro: IPR001090; -
 DR InterPro: IPR001245; -
 DR InterPro: IPR001426; -
 DR InterPro: IPR001660; -
 DR InterPro: IPR001777; -
 DR Pfam: PF01404; EPH_1bd; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00014; FNTYPE11.
 DR PRINTS: PR00109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE: PS00011; PROTEIN KINASE_DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing;
 FT SIGNAL 1 24
 FT CHAIN 1 998
 FT DOMAIN 25 556
 FT TRAMEM 577 577
 FT DOMAIN 578 998
 FT DOMAIN 192 328
 FT DOMAIN 329 438
 FT DOMAIN 439 536
 FT DOMAIN 633 894

FT DOMAIN 921 998 SAM.
 FT SITE 996 998 PDZ-BINDING MOTIF (POTENTIAL).
 FT NP_BIND 639 647 ATP (BY SIMILARITY).
 FT BINDING 665 665 ATP (BY SIMILARITY).
 FT ACT_SITE 758 758 BY SIMILARITY.
 FT MOD_RES 608 608 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 614 614 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 791 791 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 940 940 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 343 343 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 410 410 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 600 610 FPKPTKTYID -> SLVTNENLSVL (IN TRUNCATED
 FT ISOFORM).
 SQ SEQUENCE 998 AA; 111953 MW; A7A824698924876C CMC64;
 Query Match 4.1%; Score 40; DB 1; Length 998;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 775 RWTAPPAIQKRTSASDWSYGIWMEVWSYGERPYWDM 814
 DB 801 RWTAPPAIQKRTSASDWSYGIWMEVWSYGERPYWDM 840
 RESULT 9
 EPH5_CHICK
 ID EPH5_CHICK STANDARD; PRT; 1002 AA.
 AC 007497;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPHRIN TYPE-B RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 KINASE CEK9).
 GN EPHB5 OR CEK9.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9706069; PubMed-8909550;
 RA Soans C., Holash J.A., Pavlova Y., Pasquale E.B.;
 RT "Developmental expression and distinctive tyrosine phosphorylation of
 the Eph-related receptor tyrosine kinase Cek9.";
 RL J. Cell Biol. 135:781-795(1996).
 RN [2]
 RP PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE-9328394; PubMed-8510926;
 RA Sajjadi F.G., Pasquale E.B.;
 RT "Five novel avian Eph-related tyrosine kinases are differentially
 expressed.";
 RL Oncogene 8:1807-1813(1993).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THYMUS AND DETECTABLE IN
 CC BRAIN, RETINA, KIDNEY, LUNG, AND HEART. NOT DETECTED IN SKELETAL
 CC MUSCLE AND LIVER.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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CC EMBL: U23783; AAB41054.1; -
DR HSSP; P00523; 2PTK.
DR InterPro: IPR000561; -
DR InterPro: IPR000719; -
DR InterPro: IPR001090; -
DR InterPro: IPR001245; -
DR InterPro: IPR001426; -
DR InterPro: IPR001660; -
DR InterPro: IPR001777; -
DR Pfam: PF01404; EPH_Lbd; 1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS; PR00014; FNTYPEIIT.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 1 29
FT DOMAIN 30 1002 EPHRIN TYPE-B RECEPTOR 5.
FT TRANSMEM 565 585 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 586 1002 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 195 338 CYS-RICH.
FT DOMAIN 339 449 FIBRONECTIN TYPE-III.
FT DOMAIN 450 547 FIBRONECTIN TYPE-III.
FT DOMAIN 637 900 PROTEIN KINASE.
FT DOMAIN 862 865 POLY-PRO.
FT SITE 927 1002 SAM.
FT BINDING 1000 1002 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 643 651 ATP (BY SIMILARITY).
FT BINDING 669 669 ATP (BY SIMILARITY).
FT ACT_SITE 762 762 BY SIMILARITY.
FT MOD_RES 612 612 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 618 618 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 796 796 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 946 946 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC...) (POTENTIAL).
SO SEQUENCE 1002 AA; 111947 MW; 6D9635B50D8B0DA CRC64;

Query Match 3.7%; Score 36; DB 1; Length 1002;
Best Local Similarity 100.0%; Pred. No. 4.1e-30;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 723 DMNVYHDLAARNILVNSLVCKVSDFGLSRFLEDD 758
Db 755 DMNVYHDLAARNILVNSLVCKVSDFGLSRFLEDD 790

RESULT 10
EPB3_CHICK STANDARD; PRT; 988 AA.
AC 007498;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 3 (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
DE RECEPTOR CEK10) (FRAGMENT).
GN EPB3 OR CEK10.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Embryo; PubMed=8510926;
RX MEDLINE=93288394;
RA Sajjadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed."
RL Oncogene 8:1807-1813(1993).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PRESENT IN 10-DAY EMBRYONIC BRAIN AND BODY
CC TISSUES. PROMINENT EXPRESSION IN KIDNEY, LOWER EXPRESSION IN LUNG,
CC AND BARELY DETECTABLE IN BRAIN, LIVER, HEART, SKELETAL MUSCLE AND
CC THYMUS.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC -----
DR EMBL: Z19061; CAA79511.1; -
DR HSSP; P00523; 2PTK.
DR InterPro: IPR000719; -
DR InterPro: IPR001090; -
DR InterPro: IPR001245; -
DR InterPro: IPR001426; -
DR InterPro: IPR001660; -
DR InterPro: IPR001777; -
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF01404; EPH_Lbd; 1.
DR PRINTS; PR00014; FNTYPEIIT.
DR PRINTS; PR00107; PROTEIN_KINASE_ATP; 1.
DR PRINTS; PR00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Repeat.
FT NON_TER 1 1
FT DOMAIN 1 534 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 535 555 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 556 988 CYS-RICH.
FT DOMAIN 171 308 FIBRONECTIN TYPE-III.
FT DOMAIN 309 421 FIBRONECTIN TYPE-III.
FT DOMAIN 422 520 FIBRONECTIN TYPE-III.
FT DOMAIN 623 866 PROTEIN KINASE.
FT DOMAIN 913 988 SAM.
FT SITE 986 988 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 629 637 ATP (BY SIMILARITY).
FT BINDING 53 88 ATP (BY SIMILARITY).
FT BINDING 655 655 ATP (BY SIMILARITY).
FT ACT_SITE 748 748 BY SIMILARITY.
FT MOD_RES 598 598 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 604 604 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 782 782 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 932 932 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 323 323 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPPLIC 558 572 MISSING (IN SHORT ISOFORM).
SO SEQUENCE 988 AA; 109578 MW; EEA0D39C03FFD3C8 CRC64;

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Query Match 3.6%; Score 35; DB 1; Length 988;
 Best Local Similarity 100.0%; Pred. No. 4.9e-29;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 MNYVHRDLARNILVNSNLVCKVSDGLSRLFLDD 758
 DB 742 MNYVHRDLARNILVNSNLVCKVSDGLSRLFLDD 776

RESULT 11

EPB3_MOUSE STANDARD; PRT; 993 AA.
 ID EPB3_MOUSE
 AC P54754; Q62214;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR MDK-5) (DEVELOPMENTAL KINASE 5) (SEK-4).
 GN EPHB3 OR ETK2 OR MDK5 OR SEK4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Embryo;
 RX MEDLINE=96074837; PubMed=7478528;
 RA Closssek T., Lerch M.M., Ullrich A.;
 RT "Cloning, characterization, and differential expression of MDK2 and MDK5, two novel receptor tyrosine kinases of the eck/eph family.";
 RL Oncogene 11:2085-2095(1995).
 RN [2]
 RP SEQUENCE OF 719-993 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE=95034306; PubMed=7947319;
 RA Becker N., Seitandou T., Murphy P., Mattei M.G., Topilko P., Nieto A., Wilkinson D.G., Charney P., Gilardi P.;
 RT "Several receptor tyrosine kinase genes of the eph family are segmentally expressed in the developing hindbrain.";
 RL Mech. Dev. 47:3-17(1994).
 RN [3]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Tsondi R., Wiedman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors in the mouse spinal cord: a possible role in constraining the orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISK.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: Z49086; CAA88910.1; -;
 DR EMBL: X76012; CAA53599.1; -;
 DR HSSP: P00523; 2PTK.
 DR MGD: MG1:104770; Ephb3.
 DR InterPro: IPR000719; -;

DR InterPro: IPR001090; -;
 DR InterPro: IPR001245; -;
 DR InterPro: IPR001426; -;
 DR InterPro: IPR001600; -;
 DR InterPro: IPR001777; -;
 DR Pfam: PF01404; EPH_Lbd; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRINTS: PR00104; FNYPKELIT.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00790; RICEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RICEPTOR_TYR_KIN_V_2; 1.
 DR TRANSFERASE: Tyrosine-protein kinase: ATP-binding, Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 29
 FT CHAIN 30 993
 FT DOMAIN 30 554
 FT TRANSMEM 555 575
 FT DOMAIN 576 593
 FT DOMAIN 191 328
 FT DOMAIN 329 443
 FT DOMAIN 444 539
 FT DOMAIN 628 891
 FT DOMAIN 918 993
 FT SITE 991 993
 FT NE_BIND 634 642
 FT BINDING 660 660
 FT ACT_SITE 753 753
 FT MOD_RES 603 603
 FT MOD_RES 509 509
 FT MOD_RES 787 787
 FT MOD_RES 937 937
 FT CARBOHYD 343 343
 FT CARBOHYD 440 440
 FT CONFLICT 719 719
 SQ SEQUENCE 993 AA; 109585 MW; 0B66A4D391266C79 CRC64;

Query Match 3.6%; Score 35; DB 1; Length 993;
 Best Local Similarity 100.0%; Pred. No. 4.9e-29;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 MNYVHRDLARNILVNSNLVCKVSDGLSRLFLDD 758
 DB 742 MNYVHRDLARNILVNSNLVCKVSDGLSRLFLDD 781

RESULT 12

EPB3_HUMAN STANDARD; PRT; 998 AA.
 ID EPB3_HUMAN
 AC P54753;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR HEK-2).
 GN EPHB3 OR ETK2 OR HEK2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Embryo;
 RX MEDLINE=93390963; PubMed=8397371;
 RA Boehme B., Holtlich U., Wolf G., Grzeschik K.-H., Streibhardt K., Ruesamen-Waigmann H.;
 RT "PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.";

CC RT Oncogene 8:2857-2862(1993).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
 CC EPHRIN-B1 AND -B2.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X75208; CAA53021.1; -
 CC HSSP: P00523; 2PTK.
 CC DR MIM: 601839; -
 CC DR InterPro: IPR000719; -
 CC DR InterPro: IPR001090; -
 CC DR InterPro: IPR001245; -
 CC DR InterPro: IPR001426; -
 CC DR InterPro: IPR001660; -
 CC DR InterPro: IPR001777; -
 CC DR Pfam: PF01404; EPH_1bd; 1.
 CC DR Pfam: PF00536; SAM; 1.
 CC DR Pfam: PF00041; fn3; 2.
 CC DR Pfam: PF00069; pkinase; 1.
 CC DR PRINTS: PRO0014; ENTPEIIT.
 CC DR PRINTS: PRO0109; TYRKINASE.
 CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 CC DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 CC DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 CC DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 CC KM Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 CC FT STGNL 1 33
 CC FT CHAIN 34 998
 CC FT DOMAIN 34 559
 CC FT TRANSMEM 560 580
 CC FT DOMAIN 581 998
 CC FT DOMAIN 199 336
 CC FT DOMAIN 337 448
 CC FT DOMAIN 449 544
 CC FT DOMAIN 633 896
 CC FT DOMAIN 923 998
 CC FT SITE 996 998
 CC FT NE_BIND 639 647
 CC FT BINDING 665 665
 CC FT ACT_SITE 758 758
 CC FT MOD_RES 608 608
 CC FT MOD_RES 614 614
 CC FT MOD_RES 792 792
 CC FT MOD_RES 942 942
 CC FT CARBOHYD 351 351
 CC FT CARBOHYD 445 445
 CC SQ SEQUENCE 998 AA: 110286 MW: 576826397CC61103 CRC64;

Query Match 3.6%; Score 35; DB 1; Length 998;
 Best Local Similarity 100.0%; Pred No. 4.9e-29;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 MNYVHRDLAARNILVNSLVCKVSDFGSLRFLDD 758
 DB 752 MNYVHRDLAARNILVNSLVCKVSDFGSLRFLDD 786

RESULT 13
 ID EBP3_XENLA STANDARD; PRT; 974 AA.
 AC 091735;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR TCK).
 GN TCK.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP MEDLINE=96068901; PubMed=7478602;
 RA Scales J.B., Wanning R.S., Renaud C.S., Shea L.J., Sargent T.D.;
 RT "Novel members of the eph receptor tyrosine kinase subfamily expressed
 RT during Xenopus development";
 RL Oncogene 11:1745-1752(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN PRE-SOMITIC
 CC MESODERM, CAUDAL SOMITES, MIDBRAIN, AND CEMENT GLAND. MOST
 CC ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER LEVELS
 CC IN INTESTINE, KIDNEY, OVIDUCT AND PHARYNX.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: LA3620; AA03526.1; -
 CC HSSP: P29323; 1BAP.
 CC DR InterPro: IPR000719; -
 CC DR InterPro: IPR001090; -
 CC DR InterPro: IPR001245; -
 CC DR InterPro: IPR001426; -
 CC DR InterPro: IPR001660; -
 CC DR InterPro: IPR001777; -
 CC DR Pfam: PF00041; fn3; 2.
 CC DR Pfam: PF00069; pkinase; 1.
 CC DR Pfam: PF00536; SAM; 1.
 CC DR Pfam: PF01404; EPH_1bd; 1.
 CC DR PRINTS: PRO0014; ENTPEIIT.
 CC DR PRINTS: PRO0109; TYRKINASE.
 CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 CC DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 CC DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 CC DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 CC KM Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 CC FT STGNL 1 16
 CC FT CHAIN 17 974
 CC FT DOMAIN 17 534
 CC FT TRANSMEM 535 555
 CC FT DOMAIN 556 974
 CC FT DOMAIN 178 315
 CC CYTOPLASMIC (POTENTIAL).
 CC CYS-RICH.

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FT DOMAIN 316 423 FIBRONECTIN TYPE-III.
FT DOMAIN 424 520 FIBRONECTIN TYPE-III.
FT DOMAIN 609 872 FIBRONECTIN TYPE-III.
FT DOMAIN 899 974 SAM.
FT SITE 972 974 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 615 623 ATP (BY SIMILARITY).
FT DISULFID 60 95 BY SIMILARITY.
FT BINDING 641 641 ATP (BY SIMILARITY).
FT ACT_SITE 734 734 BY SIMILARITY.
FT MOD_RES 584 584 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 590 590 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 768 768 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 918 918 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 330 330 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 974 AA; 108263 MW; F881412E86628533 CRC64;

Query Match 3.4%; Score 33; DB 1; Length 974;
Best Local Similarity 100.0%; Pred. No. 7e-27;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 MNYVHRDLAARNILVNSLVCVSDGSLRFL 756
DB 728 MNYVHRDLAARNILVNSLVCVSDGSLRFL 760

RESULT 14
EPI1_CHICK
ID EPI1_CHICK STANDARD; PRT; 984 AA.
AC 007494;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 1 (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
DE RECEPTOR EPH-2) (TYROSINE KINASE CEK6 RECEPTOR) (FRAGMENT).
GN EPHB1 OR CEK6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=93288394; PubMed=8510926;
RT Sajjadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed.";
RT Oncogene 8:1807-1813(1993).
RL -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
CC EPHRIN-B1, -B2 AND -B3. MAY BE INVOLVED IN CELL-CELL INTERACTIONS
CC IN THE NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE 10-DAY EMBRYO,
CC AND IN ADULT BRAIN, LUNG, HEART AND SKELETAL MUSCLE. LOW LEVELS OF
CC EXPRESSION DETECTED IN ALL OTHER ADULT TISSUES TESTED.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; Z19110; CAA79526.1; -

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DR HSP: P00523; 2PTR.
DR InterPro: IPR000561; -.
DR InterPro: IPR000719; -.
DR InterPro: IPR001090; -.
DR InterPro: IPR001245; -.
DR InterPro: IPR001426; -.
DR InterPro: IPR001660; -.
DR InterPro: IPR001777; -.
DR Pfam: PF01404; EPH_1bd; 1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF00041; In3; 2.
DR Pfam: PF00069; pkinase; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; PARTIAL.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR TRANSFERASE: Tyrosine-protein kinase; Arp-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Repeat.
FT NON_TER 1 1
FT DOMAIN 542 552 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 542 552 POTENTIAL.
FT DOMAIN 563 984 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 164 390 CYS-RICH.
FT DOMAIN 301 410 FIBRONECTIN TYPE-III.
FT DOMAIN 411 527 FIBRONECTIN TYPE-III.
FT DOMAIN 619 882 PROTEIN KINASE.
FT DOMAIN 909 984 SAM.
FT SITE 982 984 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 625 633 ATP (BY SIMILARITY).
FT BINDING 651 651 ATP (BY SIMILARITY).
FT ACT_SITE 744 744 BY SIMILARITY.
FT MOD_RES 594 594 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 600 600 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 778 778 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 928 928 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 984 AA; 109519 MW; EF06C83BB63A13A1 CRC64;

Query Match 3.3%; Score 32; DB 1; Length 984;
Best Local Similarity 100.0%; Pred. No. 8.6e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 LDFSLRNDGQFTVLDVGLKGIAGMKYLA 722
DB 705 LDFSLRNDGQFTVLDVGLKGIAGMKYLA 736

RESULT 15
EPI1_HUMAN
ID EPI1_HUMAN STANDARD; PRT; 984 AA.
AC P54762; O43569; O95142; O95143;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EPH-2) (NET) (HEK6) (ELK).
GN EPHB1 OR EPHB2 OR NET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM EPHB1A).
RC TISSUE=Fetal brain;
RA MEDLINE=96115594; PubMed=8666391;
RA Tang X.X., Biegel J.A., Nycum L.M., Yoshioka A., Brodeur G.M.,
RA Pleasure D.E., Ikegaki N.;
RT "cDNA cloning, molecular characterization, and chromosomal
RT localization of NET(EPHB2), a human Eph-related receptor protein-
RT tyrosine kinase gene preferentially expressed in brain.";
RL Genomics 29:426-437(1995).

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RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS EPHB1A TO EPHB1D).
RC TISSUE-Kidney;
RA Stein E., Schoeckmann H.O., Daniel T.O.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP INTERACTIONS WITH GRB2 AND GRB10.
RX MEDLINE-96394464; PubMed-8798570;
RA Stein E., Cerretti D.P., Daniel T.O.;
RT Ligand activation of Elk receptor tyrosine kinase promotes its
  association with Grb10 and Grb2 in vascular endothelial cells.;
RL J. Biol. Chem. 271:23588-23593(1996).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
  EPHRIN-B1, -B2 AND -B3. MAY BE INVOLVED IN CELL-CELL INTERACTIONS
  IN THE NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
  PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBUNIT: THE LIGAND-ACTIVATED FORM INTERACTS WITH GRB2, GRB10 AND
  BINDS EPHB1 THROUGH TYR-928, WHILE GRB2 BINDS RESIDUES WITHIN THE
  CATALYTIC DOMAIN. THE NCK SH2 DOMAIN BINDS EPHB1 THROUGH TYR-594.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; EPHB1A (SHOWN HERE), EPHB1B,
  EPHB1C AND EPHB1D. ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN BRAIN.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
  RECEPTOR SUBFAMILY.
CC -----
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  or send an email to license@sib-sib.ch).
CC -----
DR EMBL; L40636; AAB08520.1; -.
DR EMBL; AF037331; AAD02030.1; -.
DR EMBL; AF037332; AAD02031.1; -.
DR EMBL; AF037333; AAB94627.1; -.
DR EMBL; AF037334; AAB94628.1; -.
DR HSP; P00523; 2PTK.
DR MIM; 600600; -.
DR InterPro; IPR000561; -.
DR InterPro; IPR000719; -.
DR InterPro; IPR001090; -.
DR InterPro; IPR001245; -.
DR InterPro; IPR001426; -.
DR InterPro; IPR001660; -.
DR InterPro; IPR001777; -.
DR Pfam; PF01404; EPH_1bd; 1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00014; ENTPEPIL.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
  Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 984 EPHRIN TYPE-B RECEPTOR 1.
FT DOMAIN 18 540 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 541 563 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 564 984 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 183 319 CYS-RICH.

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FT DOMAIN 320 429 FIBRONECTIN TYPE-III.
FT DOMAIN 430 527 FIBRONECTIN TYPE-III.
FT DOMAIN 619 882 PROTEIN KINASE.
FT DOMAIN 909 984 SAM.
FT SITE 982 984 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 625 633 ATP (BY SIMILARITY).
FT BINDING 651 651 ATP (BY SIMILARITY).
FT ACT_SITE 744 744 BY SIMILARITY.
FT MOD_RES 594 594 PHOSPHORYLATION (AUTO-).
FT MOD_RES 600 600 PHOSPHORYLATION (AUTO-).
FT MOD_RES 778 778 PHOSPHORYLATION (AUTO-).
FT MOD_RES 928 928 PHOSPHORYLATION (AUTO-).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 480 480 MALDYLILLLASVAMEETLMDTRT -> METREKKRSR
FT VASPLIC 1 27 AERGT (IN ISOFORM EPHB1B).
FT VASPLIC 617 984 MISSING (IN ISOFORM EPHB1D).
FT VASPLIC 642 682 MISSING (IN ISOFORM EPHB1C).
FT CONFLICT 12 12 A -> E (IN REF. 2).
FT CONFLICT 87 87 T -> S (IN REF. 2).
FT CONFLICT 152 152 G -> R (IN REF. 2).
FT CONFLICT 185 185 S -> I (IN REF. 2).
FT CONFLICT 274 274 T -> R (IN REF. 2).
FT CONFLICT 336 336 T -> S (IN REF. 2).
FT CONFLICT 367 367 R -> G (IN REF. 2).
FT CONFLICT 485 485 R -> S (IN REF. 2).
FT CONFLICT 813 813 V -> H (IN REF. 2).
FT CONFLICT 819 819 S -> Y (IN REF. 2).
FT CONFLICT 847 847 M -> T (IN REF. 2).
FT CONFLICT 973 973 R -> W (IN REF. 2).
SQ SEQUENCE 984 AA; 109884 MW; 8044160E24E93A92 CRC64;

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Query Match 3.3%; Score 32; DB 1; Length 984;
Best Local Similarity 100.0%; Pred. No. 8.6e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0;
QY 691 LDSELRNDGQFTVYIQLVGMRLGIAAGKXYLA 722
Db 705 LDSELRNDGQFTVYIQLVGMRLGIAAGKXYLA 736

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Search completed: July 24, 2001, 16:36:54
 Job time: 205 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:33:04 ; Search time 34.37 Seconds
(without alignments)
3733.950 Million cell updates/sec

Title: US-09-378-759-11

Sequence: 1 LIAAVEETIMDSTTATBELG.....IINSTQVMPAQMNIQSVSEV 970

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_UNCLASSIFIED:*
13: SP_VERTEBRATE:*
14: SP_VIRUS:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	322	33.2	994	11	Q9GVY4 mus sp. neu
2	296	30.5	552	4	Q9H4H4 Q9H4H4 homo sapien
3	295	30.4	621	4	Q9H4H3 Q9H4H3 homo sapien
4	54	5.6	815	13	Q9H4H3 Q9H4H3 homo sapien
5	47	4.8	353	13	Q9PVV2 lampetra re
6	40	4.1	353	13	Q9PSK9 Q9PSK9 gallus sp.
7	39	4.0	353	13	Q9U8W2 Q9U8W2 mus musculus
8	35	3.6	938	11	Q60669 Q60669 mus musculus
9	31	3.2	880	13	Q73875 Q73875 brachydanio
10	30	3.1	987	13	Q73875 Q73875 brachydanio
11	29	3.0	323	13	Q91734 Q91734 xenopus lae
12	29	3.0	976	13	Q73878 Q73878 brachydanio
13	29	3.0	977	13	Q9PWR5 Q9PWR5 xenopus lae
14	28	2.9	334	4	Q9U564 Q9U564 homo sapien
15	21	2.2	57	13	Q91564 Q91564 xenopus lae
16	20	2.1	490	13	Q73877 Q73877 brachydanio
17	19	2.0	353	13	Q9U8V9 Q9U8V9 eptatretus
18	19	2.0	853	4	Q9P269 Q9P269 homo sapien
19	19	2.0	1005	4	Q9NUA9 Q9NUA9 homo sapien

20	18	1.9	348	13	Q9U8W0 Q9U8W0 eptatretus
21	17	1.8	349	13	Q9U8W1 Q9U8W1 eptatretus
22	17	1.8	350	13	Q9PVV1 Q9PVV1 lampetra re
23	16	1.6	983	4	Q9H2V4 Q9H2V4 homo sapien
24	15	1.5	57	11	Q61821 Q61821 mus musculus
25	15	1.5	977	11	Q9ESJ2 Q9ESJ2 mus musculus
26	14	1.4	74	11	Q62128 Q62128 mus musculus
27	14	1.4	390	5	Q9U8V8 Q9U8V8 branchiostoma
28	14	1.4	1035	5	Q9XZL6 Q9XZL6 drosophila
29	14	1.4	1047	5	Q917D4 Q917D4 drosophila
30	14	1.4	1080	5	Q9Y1J0 Q9Y1J0 drosophila
31	14	1.4	1096	5	Q9V4E5 Q9V4E5 drosophila
32	13	1.3	342	5	Q9U8V7 Q9U8V7 branchiostoma
33	13	1.3	666	13	Q73876 Q73876 brachydanio
34	13	1.3	893	5	Q9Y1Y3 Q9Y1Y3 ephydatia f
35	13	1.3	1019	5	Q96435 Q96435 drosophila
36	13	1.3	1126	13	Q9PPN6 Q9PPN6 cyprinus ca
37	12	1.2	57	13	Q91999 Q91999 xenopus lae
38	12	1.2	62	5	Q61292 Q61292 anthocidari
39	12	1.2	67	5	Q25192 Q25192 hydra attenu
40	12	1.2	237	5	Q25196 Q25196 hydra attenu
41	12	1.2	435	4	Q15850 Q15850 homo sapien
42	12	1.2	465	4	Q16176 Q16176 homo sapien
43	12	1.2	465	11	P70223 P70223 mus musculus
44	12	1.2	503	4	Q15250 Q15250 homo sapien
45	12	1.2	511	11	Q64103 Q64103 mus musculus

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	994 AA.
Q9GVY4	Q9GVY4			
AC	Q9GVY4			
DT	01-MAY-2000 (TRENDEL, 13, last sequence update)			
DT	01-MAY-2000 (TRENDEL, 13, last sequence update)			
DE	01-MAR-2001 (TRENDEL, 16, last annotation update)			
DE	NEURAL KINASE, NUK=EPH/ELK FAMILY RECEPTOR-LIKE TYROSINE KINASE.			
OS	Mus sp.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10095;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94181250; PubMed=8134103;			
RA	Henkemeyer M., Marengere L.E., McGlade J., Olivier J.P., Conlon R.A.,			
RA	Holmward D.P., Letwin K., Pawson T.;			
RT	"Immunolocalization of the Nuk receptor tyrosine kinase suggests roles			
RT	in segmental patterning of the brain and axonogenesis.";			
CC	Oncogene 9:1001-1014(1994).			
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN			
CC	TYROSINE PHOSPHATE (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN			
CC	RECEPTOR SUBFAMILY.			
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
DR	HSSP; P06239; 31CK.			
DR	InterPro; IPR000561; -			
DR	InterPro; IPR000719; -			
DR	InterPro; IPR001090; -			
DR	InterPro; IPR001245; -			
DR	InterPro; IPR001426; -			
DR	InterPro; IPR001660; -			
DR	InterPro; IPR001777; -			
DR	pfam; PF00041; fn3; 2.			
DR	pfam; PF00069; pkase; 1.			
DR	pfam; PF00536; SAM; 1.			
DR	pfam; PF01404; EPH_1bc; 1.			
DR	PRINTS; PR00014; ENTPEPIL1.			
DR	PRINTS; PR00109; TYRKINASE.			
DR	PRINTS; PS01186; EGF_2; UNKNOWN 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR SMART: SM00454; SAM; 1.
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 994 AA; 110759 MW; BC6B9B12A070394C CRC64.

Query Match 33.2%; Score 322; DB 11; Length 994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 GFLYAFODYGGCSLJAVRVYRKCPRIIONGAIFOETISGAEISTLVAARGSCIANAE 218
DB 181 GFLYAFODYGGCSLJAVRVYRKCPRIIONGAIFOETISGAEISTLVAARGSCIANAE 240
QY 219 VDPPIKLYCGDDEMLVPIGRCKCKAGFEAVENGTCRCGPGSTFRANOGDEACTHCPI 278
DB 241 VDPPIKLYCGDDEMLVPIGRCKCKAGFEAVENGTCRCGPGSTFRANOGDEACTHCPI 300
QY 279 SRTTSGATNCVCRNGYRRADLPDLPCTTISAPQAVISSVNETSLMEWTPPRDSG 338
DB 301 SRTTSGATNCVCRNGYRRADLPDLPCTTISAPQAVISSVNETSLMEWTPPRDSG 360
QY 339 REDLVYNIICKSCGSGRACRCGDNVQYAPROLGLEPRITYSDLLAHTQYTFEIOAVN 398
DB 361 REDLVYNIICKSCGSGRACRCGDNVQYAPROLGLEPRITYSDLLAHTQYTFEIOAVN 420
QY 399 GVTDOSESPQFASVNTTQOAPSAVSIMHOYSRTVDSITLSNOSPDPONGVILDELO 458
DB 421 GVTDOSESPQFASVNTTQOAPSAVSIMHOYSRTVDSITLSNOSPDPONGVILDELO 480
QY 459 YRKELSEYNATAIKSPNTVT 480
DB 481 YRKELSEYNATAIKSPNTVT 502

RESULT 2
Q94H4 PRELIMINARY; PRT; 552 AA.
AC Q94H4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE D074M1.1.1 (TYROSINE KINASE ISOFORM 1) (FRAGMENT).
GN EPHB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bagguley C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL035704; CAC10350.1;
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 552 AA; 62206 MW; D643D1C857B1A3DB CRC64;

Query Match 30.5%; Score 296; DB 4; Length 552;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 574 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEVCSGHLKLPGRKEIF 633
DB 156 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEVCSGHLKLPGRKEIF 215
QY 634 VAITKLSGTEKORDFLSEASIMGOFDHPNVIHLEGVYTKSPVVIITEFMENGLDS 693
DB 216 VAITKLSGTEKORDFLSEASIMGOFDHPNVIHLEGVYTKSPVVIITEFMENGLDS 275

QY 694 FLRONDGQFTYIOLVGMILGIAAGKYLADNMYVHRDLAARILVNSNLYCKVSPFGLSR 753
DB 276 FLRONDGQFTYIOLVGMILGIAAGKYLADNMYVHRDLAARILVNSNLYCKVSPFGLSR 335
QY 754 FLEDDTSPTYSALGKRPIMTAPALQYRKFTSASDVMSYGIWMEMVSGERYWD 813
DB 336 FLEDDTSPTYSALGKRPIMTAPALQYRKFTSASDVMSYGIWMEMVSGERYWD 395
QY 814 MTNODVINAIEDYELPPMDCPSALHQLMDCWKDRNRHRCFQIYNTLDKMRNPS 873
DB 396 MTNODVINAIEDYELPPMDCPSALHQLMDCWKDRNRHRCFQIYNTLDKMRNPS 455
QY 874 LKAMAPLSSGINLPIDRTIPDYTSFNVDWMLFAIKMGQYKESFANAGFTSFVVSQMM 933
DB 456 LKAMAPLSSGINLPIDRTIPDYTSFNVDWMLFAIKMGQYKESFANAGFTSFVVSQMM 515
QY 934 MEDILRVGVTLAGHCKILNSIQVMRAQNOIQSVEV 970
DB 516 MEDILRVGVTLAGHCKILNSIQVMRAQNOIQSVEV 552

RESULT 3
Q94H3 PRELIMINARY; PRT; 621 AA.
AC Q94H3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE D074M1.1.2 (TYROSINE KINASE ISOFORM 2) (FRAGMENT).
GN EPHB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bagguley C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL035704; CAC10351.1;
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 621 AA; 69824 MW; 3DA1DCEB04979BF CRC64;

Query Match 30.4%; Score 295; DB 4; Length 621;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 574 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEVCSGHLKLPGRKEIF 633
DB 156 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEVCSGHLKLPGRKEIF 215
QY 634 VAITKLSGTEKORDFLSEASIMGOFDHPNVIHLEGVYTKSPVVIITEFMENGLDS 693
DB 216 VAITKLSGTEKORDFLSEASIMGOFDHPNVIHLEGVYTKSPVVIITEFMENGLDS 275
QY 694 FLRONDGQFTYIOLVGMILGIAAGKYLADNMYVHRDLAARILVNSNLYCKVSPFGLSR 753
DB 276 FLRONDGQFTYIOLVGMILGIAAGKYLADNMYVHRDLAARILVNSNLYCKVSPFGLSR 335
QY 754 FLEDDTSPTYSALGKRPIMTAPALQYRKFTSASDVMSYGIWMEMVSGERYWD 813
DB 336 FLEDDTSPTYSALGKRPIMTAPALQYRKFTSASDVMSYGIWMEMVSGERYWD 395
QY 814 MTNODVINAIEDYELPPMDCPSALHQLMDCWKDRNRHRCFQIYNTLDKMRNPS 873
DB 396 MTNODVINAIEDYELPPMDCPSALHQLMDCWKDRNRHRCFQIYNTLDKMRNPS 455
QY 874 LKAMAPLSSGINLPIDRTIPDYTSFNVDWMLFAIKMGQYKESFANAGFTSFVVSQMM 933
DB 456 LKAMAPLSSGINLPIDRTIPDYTSFNVDWMLFAIKMGQYKESFANAGFTSFVVSQMM 515

QY 934 MEDLRVGVTLGHOKILNSIQVMRAQMOIQSVE 969
DB 516 MEDLRVGVTLGHOKILNSIQVMRAQMOIQSVE 551

RESULT 4

057458 PRELIMINARY; PRT; 815 AA.
AC 057458;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE EPHB2-TYROSINE KINASE RECEPTOR (FRAGMENT).
GN XEPHB2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;

CC [1]
RN SEQUENCE FROM N.A.
RP Tanaka M., Wang D.Y., Kamo T., Igarashi H., Wang Y., Xiang Y.Y.,
RA Tanaka F., Naitoh Y., Sugimura H.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC EMBL: AB026039; AAB94603.1; -;
DR HSSP: P29323; 184F.
DR InterPro: IPR000561; -;
DR InterPro: IPR000719; -;
DR InterPro: IPR001245; -;
DR InterPro: IPR001426; -;
DR InterPro: IPR001660; -;
DR InterPro: IPR001777; -;
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00536; SAM; 1.
DR PRINTS: PRO0014; FNTYPEITI.
DR PRINTS: PRO0109; TYRKINASE.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR SMART: SM00454; SAM; 1.
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;
KW Transferrase; Transmembrane; Tyrosine-protein kinase.
FT NON_TER
SQ SEQUENCE 815 AA: 90848 MW: D36D77C498097BFE CRC64;

Query Match 5.6%; Score 54; DB 13; Length 815;
Best Local Similarity 100.0%; Pred. No. 5.6e-48;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TTPMKIYIDPFTEDPNEAVREFAKEDISCVKIEOVIGAGEGECVSGHLKLP 627
DB 419 TTPMKIYIDPFTEDPNEAVREFAKEDISCVKIEOVIGAGEGECVSGHLKLP 472

RESULT 5

09PVV2 PRELIMINARY; PRT; 353 AA.
AC 09PVV2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE EPHB (FRAGMENT).

OS Lampetra reissneri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7753;

RP SEQUENCE FROM N.A.
RX MEDLINE=20020330; PubMed=10552041;
RA Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey;
RT Isoform duplications around the divergence of cyclostomes and
RT gnathostomes".
RL J. Mol. Evol. 49:601-608(1999).
DR EMBL: AB025542; BAA84732.1; -;
DR HSSP: P06239; 3LCK.
DR InterPro: IPR000719; -;
DR InterPro: IPR001245; -;
DR InterPro: IPR001660; -;
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00536; SAM; 1.
DR PRINTS: PRO0109; TYRKINASE.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR SMART: SM00454; SAM; 1.
KW ATP-binding; Transferase; Tyrosine-protein kinase.
FT NON_TER
SQ SEQUENCE 353 AA: 39797 MW: 034B315DA02BED8D CRC64;

Query Match 4.8%; Score 47; DB 13; Length 353;
Best Local Similarity 100.0%; Pred. No. 7.2e-41;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 678 PVMIITEFMENGSIDSFRLRQNDGQFTVIQVGMIRGIAAGMKYLA DM 724
DB 61 PVMIITEFMENGSIDSFRLRQNDGQFTVIQVGMIRGIAAGMKYLA DM 107

RESULT 6
09PSK9 PRELIMINARY; PRT; 60 AA.
AC 09PSK9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROTEIN KINASE.
OS Gallus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93096482; PubMed=1281306;
RA Marcelle C., Eichmann A.;
RT "Molecular cloning of a family of protein kinase genes expressed in
RT the avian embryo".
RL Oncogene 7:2479-2487(1992).
DR HSSP: P12931; 1FMK.
DR InterPro: IPR000719; -;
DR Pfam: PF00069; pkinase; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 60 AA: 6593 MW: EA947B9C0857B243 CRC64;

Query Match 4.1%; Score 40; DB 13; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.9e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 AARNITVNSLVCKVSDFGISRLFEDTSDPYTTSALGK 771
DB 1 AARNITVNSLVCKVSDFGISRLFEDTSDPYTTSALGK 40

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RESULT 7
ID Q908W2 PRELIMINARY; PRT; 353 AA.
AC Q908W2;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE EPHB (FRAGMENT).
OC Eptarectus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotretli; Myxiniiformes;
OC Myxiniidae; Eptarectinae; Eptarectus.
OX NCBI_TaxId=7764;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20020330; PubMed=10552041.
RA Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey;
RT isoform duplications around the divergence of cyclostomes and
RT gnathostomes.";
RL J. Mol. Evol. 49:601-608(1999).
DR EMBL; AB025538; BAA84728.1; -.
DR HSSP; P00523; 2PTK.
DR InterPro; IPR00719; -.
DR InterPro; IPR001245; -.
DR InterPro; IPR001660; -.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR SMART; SM00454; SAM; 1.
DR ATP-binding; Transferase; Tyrosine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 353 AA; 39821 MW; 239E5B953698402A CRC64;

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Query Match
Best Local Similarity 100.0%; Score 39; DB 13; Length 353;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 686 MENGSLDSELRNDGQFTVQLVGMRLGIAAGKRYLADM 724
DB 69 MENGSLDSELRNDGQFTVQLVGMRLGIAAGKRYLADM 107

RESULT 8
ID Q60669 PRELIMINARY; PRT; 938 AA.
AC Q60669;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE PROTEIN KINASE (FRAGMENT).
GN EPHB3 OR ETK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteeria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95200798; PubMed=7893599;
RA Ruiz J.C., Conlon F.L., Robertson E.J.;
RT "Identification of novel protein kinases expressed in the myocardium
RT of the developing mouse heart.";
RL Mech. Dev. 48:153-164(1994).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DB EMBL; U11493; AAA67925.1; -.

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DR HSSP; P29323; 1BAF.
DR MGI; MGI:104770; Ephb3.
DR InterPro; IPR000719; -.
DR InterPro; IPR001090; -.
DR InterPro; IPR001245; -.
DR InterPro; IPR001426; -.
DR InterPro; IPR001660; -.
DR InterPro; IPR001777; -.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF01404; EPH_lbd; 1.
DR PRINTS; PR00014; ENYPEPIL.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR SMART; SM00454; SAM; 1.
DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 938 AA; 103996 MW; 8D128CA46f19e73f CRC64;

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Query Match
Best Local Similarity 100.0%; Score 35; DB 11; Length 938;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 724 MNVHRDLAARNILVNSNLVCVSDFGLSRFLEDD 758
DB 692 MNVHRDLAARNILVNSNLVCVSDFGLSRFLEDD 726

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RESULT 9
ID Q73879 PRELIMINARY; PRT; 880 AA.
AC Q73879;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE EPH-LIKE RECEPTOR TYROSINE KINASE RTK4 (FRAGMENT).
GN RTK4.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Cooke J.E.;
RT Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cooke J.E., Xu Q., Wilson S.W., Holder N.;
RX Dev. Genes Evol. 206:515-531(1997).
RL -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DB EMBL; AJ005030; CAA06303.1; -.
DR HSSP; P00523; 2PTK.
DR ZFIN; ZDB-GENE-990415-61; rtk4.
DR InterPro; IPR000561; -.
DR InterPro; IPR000719; -.
DR InterPro; IPR001090; -.
DR InterPro; IPR001245; -.
DR InterPro; IPR001426; -.
DR InterPro; IPR001660; -.
DR InterPro; IPR001777; -.

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DR Pfam: PF000041; fn3.2.
 DR PFam: PF000069; Pkinase; 1.
 DR Pfam: PF01404; Eph_Lbd; 1.
 DR PRINTS: PR00014; FNTYPEIIT.
 DR PRINTS: PR00109; TYRKINASE.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR SMART: SM00219; TYRKC; 1.
 KM ATP-binding; Glycopolymers; Phosphorylation; Receptor; Repeat;
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 880 AA; 98862 MW; 8875D13FB179B70B CRC64;

Query Match 3.2%; Score 31; DB 13; Length 880;
 Best Local Similarity 100.0%; Pred. No. 1,7e-23;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 784 YRKFTSASDVMSYGIWMEVMSYGERPYDM 814
 DB 741 YRKFTSASDVMSYGIWMEVMSYGERPYDM 771

RESULT 10
 ID 073875 PRELIMINARY; PRT; 987 AA.
 AC 073875;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE EPH-LIKE RECEPTOR TYROSINE KINASE RTK5.
 OS Brachydanio rerio (zebrafish) (Zebrafish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 NCBI_TaxID=7955;
 [1]
 RN SEQUENCE FROM N.A.
 RA COOKE J.E., Xu Q., Wilson S.W., Holder N.;
 RT "Characterisation of five novel zebrafish eph-related receptor
 RT tyrosine kinases suggests roles in patterning the neural plate."
 RL Dev. Genes Evol. 206:515-531(1997).
 [2]
 RN SEQUENCE FROM N.A.
 RA Pubmed-1171340;
 RA Cooke J.E., Moens C.B., Roth L.W.A., Durbin L., Shlomi K., Brennan C.,
 RT "Eph signalling functions downstream of Val to regulate cell sorting
 RT and boundary formation in the caudal hindbrain."
 RL Development 128:571-580(2001).
 EMBL: AJ005026; CAA06299.2; -;
 DR InterPro: IPR000719; -;
 DR InterPro: IPR001090; -;
 DR InterPro: IPR001245; -;
 DR InterPro: IPR001660; -;
 DR InterPro: IPR001777; -;
 DR Pfam: PF000041; fn3.2.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF01404; Eph_Lbd; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRODOM: PD001495; -; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR SMART: SM00454; SAM; 1.
 KM Receptor; Kinase.
 SQ SEQUENCE 987 AA; 109547 MW; 1099FC1410A84918 CRC64;

Query Match 3.1%; Score 30; DB 13; Length 987;
 Best Local Similarity 100.0%; Pred. No. 2.1e-22;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 726 YVHRDLARNILVNSNLCKVSDGLSRFL 755
 DB 742 YVHRDLARNILVNSNLCKVSDGLSRFL 771

RESULT 11
 ID 091734 PRELIMINARY; PRT; 323 AA.
 AC 091734;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE EPH RECEPTOR TYROSINE KINASE (EC 2.7.1.112) (PL7A) (FRAGMENT).
 GN G51.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 [1]
 RN SEQUENCE FROM N.A.
 RA MEDLINE-96068901; Pubmed-7478602;
 RA Sales J.B., Manning R.S., Renaud C.S., Shea L.J., Sargent T.D.;
 RT "Novel members of the eph receptor tyrosine kinase subfamily expressed
 RT during xenopus development."
 RL Oncogene 11:1745-1752(1995).
 [2]
 RN SEQUENCE OF 84-142 FROM N.A.
 RC TISSUE-EMBRYO;
 RX MEDLINE-95383727; Pubmed-7655077;
 RA Brandt A.W., Kirschner M.W.;
 RT "Molecular cloning of tyrosine kinases in the early xenopus embryo;
 RT identification of Eck-related genes expressed in cranial neural crest
 RT cells of the second (hyoid) arch."
 RL Dev. Dyn. 203:119-140(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED THROUGH THE HEAD AND IN THE TIP OF
 CC THE EMBRYO TAIL. EXTREMELY LOW AND UBIQUITOUS EXPRESSION IN ADULT
 CC TISSUES.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 DR EMBL: L43622; AAA93525.1; -;
 DR EMBL: U11728; AAA91291.1; -;
 DR HSPB; P29323; 184F.
 DR InterPro: IPR000719; -;
 DR InterPro: IPR001245; -;
 DR InterPro: IPR001660; -;
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR SMART: SM00454; SAM; 1.
 KM Transferase; Tyrosine-protein kinase; Phosphorylation.
 FT NON_TER 1
 FT NON_TER 1
 FT DOMAIN <1 219 PROTEIN KINASE.
 FT ACT_SITE 81 81 BY SIMILARITY.
 FT MOD_RES 115 115 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 323 AA; 36518 MW; C59800A76BA388B2 CRC64;

Query Match 3.0%; Score 29; DB 13; Length 323;
 Best Local Similarity 100.0%; Pred. No. 8.9e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 727 VHRDLAARNILVNSLVCKVSDGSLRFL 755
DB 78 VHRDLAARNILVNSLVCKVSDGSLRFL 106

RESULT 12
ID 073878 PRELIMINARY; PRT; 976 AA.
AC 073878;
DT 01-AUG-1998 (TREMBLERL. 07, Created)
DT 01-AUG-1998 (TREMBLERL. 07, last sequence update)
DT 01-MAR-2001 (TREMBLERL. 16, last annotation update)
DE EPH-LIKE RECEPTOR TYROSINE KINASE RTK8.
GN RTK8.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Cooke J.E., Xu Q., Wilson S.W., Holder N.;
RA Dev. Genes Evol. 206:515-531(1997).
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ005029; CA06302.1; -.
DR HSSP; P00523; 2PTK.
DR ZFIN; ZDB-GENE-990415-65; rtk8.
DR InterPro: IPR000561; -.
DR InterPro: IPR000719; -.
DR InterPro: IPR001090; -.
DR InterPro: IPR001245; -.
DR InterPro: IPR001660; -.
DR InterPro: IPR001777; -.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; PKinase; 1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF01404; EPH_Lbd; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; -.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR SMART; SM00454; SAM; 1.
DR ATP-binding; EGF-like domain; Glycoprotein; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 976 AA; 108180 MW; 4619754A38B0B1F CRC64;

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Query Match 3.0%; Score 29; DB 13; Length 976;
 Best Local Similarity 100.0%; Pred. No. 2,4e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 727 VHRDLAARNILVNSLVCKVSDGSLRFL 755
DB 735 VHRDLAARNILVNSLVCKVSDGSLRFL 763

RESULT 13
ID 09PWR5 PRELIMINARY; PRT; 977 AA.
AC 09PWR5;
DT 01-MAY-2000 (TREMBLERL. 13, Created)
DT 01-MAY-2000 (TREMBLERL. 13, last sequence update)
DT 01-MAR-2001 (TREMBLERL. 16, last annotation update)
DE EPH RECEPTOR TYROSINE KINASE PRECURSOR.
GN EPHA2.
OS Xenopus laevis (African clawed frog).

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OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99077686; PubMed=9858686;
RA Heibling P.M., Tran C.T., Brandt A.W.;
RT "Requirement for Epha receptor signaling in the segregation of Xenopus
RT third and fourth arch neural crest cells.";
RL Mech. Dev. 78:63-79(1998).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN KINASES. EPHRIN
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL; AJ002493; CA05500.1; -.
DR HSSP; P08631; IAD5.
DR InterPro: IPR000561; -.
DR InterPro: IPR000719; -.
DR InterPro: IPR001090; -.
DR InterPro: IPR001245; -.
DR InterPro: IPR001426; -.
DR InterPro: IPR001660; -.
DR InterPro: IPR001777; -.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; PKinase; 1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF01404; EPH_Lbd; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; -.
DR PROSITE; PS01186; EGF_2; UNKNOWN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR SMART; SM00454; SAM; 1.
DR ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 24 EPH RECEPTOR TYROSINE KINASE.
FT CHAIN 25 977 POTENTIAL.
SQ SEQUENCE 977 AA; 109593 MW; 9931C19031A55F1D CRC64;

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Query Match 3.0%; Score 29; DB 13; Length 977;
 Best Local Similarity 100.0%; Pred. No. 2,4e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 784 YRKFTSASDVSYGIYVMEVMSYGERPYW 812
DB 792 YRKFTSASDVSYGIYVMEVMSYGERPYW 820

RESULT 14
ID 09UF33 PRELIMINARY; PRT; 334 AA.
AC 09UF33;
DT 01-MAY-2000 (TREMBLERL. 13, Created)
DT 01-MAY-2000 (TREMBLERL. 13, last sequence update)
DT 01-MAR-2001 (TREMBLERL. 16, last annotation update)
DE HYPOTHETICAL 37.3 KDA PROTEIN.
GN DKF2P434C1418.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA OTTENVAELDER B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AL133666; CAB63775.1; -.
 DR InterPro; IPR000719; -.
 DR InterPro; IPR001245; -.
 DR Pfam; PF00069; pkinase.1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR SMART; SM00219; tyrc; 1.
 KW ATP-binding; Hypothetical protein; Transferase;
 KW Tyrosine-protein kinase.
 SQ SEQUENCE 334 AA; 37274 MW; DF89BC8423AC1A60 CRC64;

Query Match 2.9%; Score 28; DB 4; Length 334;
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 726 YVHRDLARNILVNSNLVCKVSDGFLSR 753
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 DB 280 YVHRDLARNILVNSNLVCKVSDGFLSR 307

RESULT 15
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 ID QY1564 PRELIMINARY; PRT; 57 AA.
 AC QY1564;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PROTEIN-TYROSINE KINASE (E17) (FRAGMENT).
 GN E17.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_Taxid=6355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95383727; PubMed=7655077;
 RA Brandl A.W., Kirschner M.W.;
 RT "Molecular cloning of tyrosine kinases in the early Xenopus embryo:
 RT Identification of Eek-related genes expressed in cranial neural crest
 RT cells of the second (hyoid) arch."
 RL Dev. Dyn. 203:119-140(1995).
 DR EMBL; U11721; AAA91284.1; -.
 DR InterPro; IPR000719; -.
 DR Pfam; PF00069; pkinase.1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase; Tyrosine-protein kinase.
 FT NON_TER 1
 FT 57
 SQ SEQUENCE 57 AA; 6231 MW; 7363203E6101D00 CRC64;

Query Match 2.2%; Score 21; DB 13; Length 57;
 Best Local Similarity 100.0%; Pred. No. 5.8e-14;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 733 ARNITVNSNLVCKVSDGFLSR 753
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 DB 1 ARNITVNSNLVCKVSDGFLSR 21

Search completed: July 24, 2001, 16:36:31
 Job time: 207 sec

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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:23:24 ; Search time 16.3 Seconds

(without alignments)
1198.791 Million cell updates/sec

Title: US-09-378-759-11

Perfect score: 5116
Sequence: 1 LIAAEEFLMSTRTATLGLG.....ILNSTQVMRAQMNQISVEV 970Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCNUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	5116	100.0	970	2	US-08-449-645A-11
2	5116	100.0	970	2	US-08-702-367A-11
3	5116	100.0	970	5	PCN-US95-04681-11
4	5082	99.3	994	4	US-08-542-635-2
5	4950.5	96.8	995	1	US-08-162-809-18
6	4934.5	96.5	1011	1	US-08-162-809-12
7	4919.5	96.2	995	2	US-08-673-789-5
8	3909.5	76.4	984	2	US-08-673-789-6
9	3706.5	72.4	951	1	US-08-162-809-2
10	3656	71.5	973	1	US-08-162-809-10
11	3649.5	71.3	988	1	US-08-162-809-14
12	3632.5	71.0	998	2	US-08-449-645A-20
13	3632.5	71.0	998	2	US-08-702-367A-20
14	3632.5	71.0	998	5	PCN-US95-04681-20
15	3595.5	70.3	970	2	US-08-673-789-7
16	3590.5	70.2	993	1	US-08-348-143-1
17	3590.5	70.2	993	1	US-08-571-785-1
18	3326.5	65.0	973	1	US-08-162-809-8
19	3035	59.3	986	2	US-08-673-789-3
20	3031	59.2	967	2	US-08-449-645A-30
21	3031	59.2	967	2	US-08-702-367A-30
22	3031	59.2	986	2	US-08-449-645A-15
23	3031	59.2	986	2	US-08-702-367A-15
24	3031	59.2	986	5	PCN-US95-04681-15
25	3031	59.2	991	2	US-08-449-645A-13
26	3031	59.2	991	2	US-08-702-367A-13
27	3031	59.2	991	5	PCN-US95-04681-13

28	3024	59.1	1104	1	US-08-222-616-36	Sequence 36, Appl
29	3024	59.1	1104	5	PCN-US95-04228-36	Sequence 36, Appl
30	3016	59.0	998	2	US-08-449-645A-17	Sequence 17, Appl
31	3016	59.0	998	2	US-08-702-367A-17	Sequence 17, Appl
32	3016	59.0	998	5	PCN-US95-04681-17	Sequence 17, Appl
33	3001	58.7	998	5	PCN-US96-00419-2	Sequence 21, Appl
34	2912.5	56.9	983	2	US-08-449-645A-21	Sequence 21, Appl
35	2912.5	56.9	983	2	US-08-702-367A-21	Sequence 21, Appl
36	2912.5	56.9	983	5	PCN-US95-04681-21	Sequence 16, Appl
37	2910	56.9	983	1	US-08-162-809-16	Sequence 10, Appl
38	2909.5	56.9	983	1	US-08-715-106-10	Sequence 10, Appl
39	2909.5	56.9	983	3	US-08-469-537A-103	Sequence 103, App
40	2907	56.8	1005	2	US-08-673-789-4	Sequence 4, Appl
41	2902.5	55.7	982	2	US-08-436-044-6	Sequence 6, Appl
42	2827.5	55.3	987	1	US-08-436-054-6	Sequence 6, Appl
43	2827.5	55.3	987	2	PCN-US95-08812-6	Sequence 6, Appl
44	2827.5	55.3	987	5	US-08-222-616-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-449-645A-11
Sequence 11, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: FOX, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-11

Query Match 100.0%; Score 5116; DB 2; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAAEEFLMSTRTATLGLG.....ILNSTQVMRAQMNQISVEV 970
DB 1 LIAAEEFLMSTRTATLGLG.....ILNSTQVMRAQMNQISVEV 970
QY 61 TKFIRRAHIIHVMKRSVDCSSIPSPGSKETFLNYEADPDSATKTFPNMNP 120
DB 61 TKFIRRAHIIHVMKRSVDCSSIPSPGSKETFLNYEADPDSATKTFPNMNP 120
QY 121 WKVDFTIADSFSSVDLGGVNMKINTEVRSFGPVSRSGLFLAODYGGCSILIAVAVFY 180

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Db 121 WKVDTIADESFQVDLGGRYMKINTEVRSFGVSRSGFYLAFOYGGCMLIAVRFEY 180
QY 181 RKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDDEMLVPIGR 240
Db 181 RKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDDEMLVPIGR 240
QY 241 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSEGATNCVCNRYRADL 300
Db 241 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSEGATNCVCNRYRADL 300
QY 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
Db 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
QY 361 CGDNQOYAPROGLTEPRITVSDLAHTQYTFEIOAVNGVVDQSPFSQFASVNTTNOA 420
Db 361 CGDNQOYAPROGLTEPRITVSDLAHTQYTFEIOAVNGVVDQSPFSQFASVNTTNOA 420
QY 421 APSAVSIMHOVSRTVDSITLISMSQPDQPNQVILDELOYYEKELSEYNATAIKSPNTVT 480
Db 421 APSAVSIMHOVSRTVDSITLISMSQPDQPNQVILDELOYYEKELSEYNATAIKSPNTVT 480
QY 481 GLKAGAIYFQVRAATYAGVGRYSKMYEOTMTEAEVOTSTOEKPLILIGSSAGLVFLI 540
Db 481 GLKAGAIYFQVRAATYAGVGRYSKMYEOTMTEAEVOTSTOEKPLILIGSSAGLVFLI 540
QY 541 AVVVAIYVNCNRGFERADSEYTDKLOHTSGHITPGMKIYIDPPTYEDPNAVAREFAKEI 600
Db 541 AVVVAIYVNCNRGFERADSEYTDKLOHTSGHITPGMKIYIDPPTYEDPNAVAREFAKEI 600
QY 601 DISCVKIEOYVIGAGEFEGVCSGHLKLPGRKEIFAIAITLKSGETEKORDFLSEASIMQ 660
Db 601 DISCVKIEOYVIGAGEFEGVCSGHLKLPGRKEIFAIAITLKSGETEKORDFLSEASIMQ 660
QY 661 FDHENVIHLEBGVYTKSPVMIITEFMENGSLDSPLRONDQOFTYIOVGLRGIAAGMKY 720
Db 661 FDHENVIHLEBGVYTKSPVMIITEFMENGSLDSPLRONDQOFTYIOVGLRGIAAGMKY 720
QY 721 LADMNYVHRDLAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTYTALGCKPFRMTAPE 780
Db 721 LADMNYVHRDLAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTYTALGCKPFRMTAPE 780
QY 781 AIORYKFTSASDVWSYGIWVEMWMSYGERPYMNTODVYNALEODYRLPPMDCSALH 840
Db 781 AIORYKFTSASDVWSYGIWVEMWMSYGERPYMNTODVYNALEODYRLPPMDCSALH 840
QY 841 QLMIDCWQKDRNHRPFQGLVNTLDKMRNPSLAKAAPLSSGINTPLDRTIPDTSFN 900
Db 841 QLMIDCWQKDRNHRPFQGLVNTLDKMRNPSLAKAAPLSSGINTPLDRTIPDTSFN 900
QY 901 TYDEMLEAIKMGYKESFANAGTSEFVVSQMMEDILRVGVTLAGHOKKIINSIQVRA 960
Db 901 TYDEMLEAIKMGYKESFANAGTSEFVVSQMMEDILRVGVTLAGHOKKIINSIQVRA 960
QY 961 QMNOIOSVEV 970
Db 961 QMNOIOSVEV 970

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RESULT 2
US-08-702-367A-11
; Sequence 11, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RMW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks

```

```

; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-367A-11

```

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Query Match 100.0%; Score 5116; DB 2; Length 970;
Best local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LLAABETLMDSTTAAELGMYVHPSPGWEVEVSGYDENNTIRTYOVNVPSSQNNMLR 60
Db 1 LLAABETLMDSTTAAELGMYVHPSPGWEVEVSGYDENNTIRTYOVNVPSSQNNMLR 60
QY 61 TKFIRRGARHRIHVEKKEFVRCDSSTIPSVGCKEFTFNLYYEADPDSATKTFPMMEHP 120
Db 61 TKFIRRGARHRIHVEKKEFVRCDSSTIPSVGCKEFTFNLYYEADPDSATKTFPMMEHP 120
QY 121 WKVDTIADESFQVDLGGRYMKINTEVRSFGVSRSGFYLAFOYGGCMLIAVRFEY 180
Db 121 WKVDTIADESFQVDLGGRYMKINTEVRSFGVSRSGFYLAFOYGGCMLIAVRFEY 180
QY 181 RKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDDEMLVPIGR 240
Db 181 RKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDDEMLVPIGR 240
QY 241 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSEGATNCVCNRYRADL 300
Db 241 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSEGATNCVCNRYRADL 300
QY 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
Db 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
QY 361 CGDNQOYAPROGLTEPRITVSDLAHTQYTFEIOAVNGVVDQSPFSQFASVNTTNOA 420
Db 361 CGDNQOYAPROGLTEPRITVSDLAHTQYTFEIOAVNGVVDQSPFSQFASVNTTNOA 420
QY 421 APSAVSIMHOVSRTVDSITLISMSQPDQPNQVILDELOYYEKELSEYNATAIKSPNTVT 480
Db 421 APSAVSIMHOVSRTVDSITLISMSQPDQPNQVILDELOYYEKELSEYNATAIKSPNTVT 480
QY 481 GLKAGAIYFQVRAATYAGVGRYSKMYEOTMTEAEVOTSTOEKPLILIGSSAGLVFLI 540
Db 481 GLKAGAIYFQVRAATYAGVGRYSKMYEOTMTEAEVOTSTOEKPLILIGSSAGLVFLI 540
QY 541 AVVVAIYVNCNRGFERADSEYTDKLOHTSGHITPGMKIYIDPPTYEDPNAVAREFAKEI 600
Db 541 AVVVAIYVNCNRGFERADSEYTDKLOHTSGHITPGMKIYIDPPTYEDPNAVAREFAKEI 600
QY 601 DISCVKIEOYVIGAGEFEGVCSGHLKLPGRKEIFAIAITLKSGETEKORDFLSEASIMQ 660
Db 601 DISCVKIEOYVIGAGEFEGVCSGHLKLPGRKEIFAIAITLKSGETEKORDFLSEASIMQ 660
QY 661 FDHENVIHLEBGVYTKSPVMIITEFMENGSLDSPLRONDQOFTYIOVGLRGIAAGMKY 720

```

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Db 661 FDHPNVTHLEGVYTKSPVMIITEFMENGSLDSFLRQNDGQFTVIOVLGMLGIAAGMKY 720
Qy 721 LADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDOTSDPTYSALGKFPRTWTAPE 780
Db 721 LADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDOTSDPTYSALGKFPRTWTAPE 780
Qy 781 AIOYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNDVINAIEODYRLPPMDCCPSALH 840
Db 781 AIOYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNDVINAIEODYRLPPMDCCPSALH 840
Qy 841 QLMIDCQOKDRNHRPKFGQIVNTLDKMIIRNPNSLKAMAPLSSGILNPLDRTIPDYTSFN 900
Db 841 QLMIDCQOKDRNHRPKFGQIVNTLDKMIIRNPNSLKAMAPLSSGILNPLDRTIPDYTSFN 900
Qy 901 TVDWMLEAIKMGQYKESFANAGFTSFVVSQMMMEDILRVGVTLAGHOKKILNSIOVMRA 960
Db 901 TVDWMLEAIKMGQYKESFANAGFTSFVVSQMMMEDILRVGVTLAGHOKKILNSIOVMRA 960
Qy 961 QMNOIOSVEV 970
Db 961 QMNOIOSVEV 970

```

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RESULT 3
PCT-US95-04681-11
Sequence 11, Application PC/TUS9504681
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBM
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-11

```

```

Query Match 100.0%; Score 5116; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LAAVEETLMSTATAELGMMVHPGSGMEVSGYDENMNTIRIYOVCNFESSQNMWLR 60
Db 1 LAAVEETLMSTATAELGMMVHPGSGMEVSGYDENMNTIRIYOVCNFESSQNMWLR 60
Qy 61 TKFTRRRAAHIIHYEMKFSVADCSIPSPGCKETENLYLYEADFDSATKTTPNMWENP 120
Db 61 TKFTRRRAAHIIHYEMKFSVADCSIPSPGCKETENLYLYEADFDSATKTTPNMWENP 120
Qy 121 WVKVDITIADESQVDLGGVHKINTEVRSFGVSHSGYTLAFQDYGGCMLIAVRVFI 180

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Db 121 WVKVDITIADESQVDLGGVHKINTEVRSFGVSHSGYTLAFQDYGGCMLIAVRVFI 180
Qy 181 RRCPRITONGAIFOETLSAESTSLVAARGSCIANAEEDVPITKYCGDDEMLVPIGRC 240
Db 181 RRCPRITONGAIFOETLSAESTSLVAARGSCIANAEEDVPITKYCGDDEMLVPIGRC 240
Qy 241 MCKAGEAVENTVRCGDSGTFFKANOGDEACTHCPIINSRTTSEGATNCVCNRYRADL 300
Db 241 MCKAGEAVENTVRCGDSGTFFKANOGDEACTHCPIINSRTTSEGATNCVCNRYRADL 300
Qy 301 DPLDMPCCTIPSPAPAVISSVNETSLMLEMTPRPSGSGREDLVYNIITCKSCSGRGACTR 360
Db 301 DPLDMPCCTIPSPAPAVISSVNETSLMLEMTPRPSGSGREDLVYNIITCKSCSGRGACTR 360
Qy 361 CGDNQVAPROLGLTEPRITYSIDLAAHTQYTFEIOAVNGVTDQSPSPFASVITITNOA 420
Db 361 CGDNQVAPROLGLTEPRITYSIDLAAHTQYTFEIOAVNGVTDQSPSPFASVITITNOA 420
Qy 421 APSAVSIMHOVSRTVDSITLSMSQPDQNGVILDYELQYEBELSEYNATAIKSPNTVT 480
Db 421 APSAVSIMHOVSRTVDSITLSMSQPDQNGVILDYELQYEBELSEYNATAIKSPNTVT 480
Qy 481 GLKAGAIYFQVRAATVAGYGRYSGKMVFQMTPEAYOTSIOEKLPLITGSSAAGLVFLI 540
Db 481 GLKAGAIYFQVRAATVAGYGRYSGKMVFQMTPEAYOTSIOEKLPLITGSSAAGLVFLI 540
Qy 541 AVVYAIACNRRGERADSETYTDKLOHTSGHTPGMKIYIDPFYEDPNEAVREFAKEL 600
Db 541 AVVYAIACNRRGERADSETYTDKLOHTSGHTPGMKIYIDPFYEDPNEAVREFAKEL 600
Qy 601 DISCVKIEOVIGAGEFGEVCSGHILKPGKREIFVAILTKSGYTEORORPFLSEASIMGO 660
Db 601 DISCVKIEOVIGAGEFGEVCSGHILKPGKREIFVAILTKSGYTEORORPFLSEASIMGO 660
Qy 661 FDHPNVTHLEGVYTKSPVMIITEFMENGSLDSFLRQNDGQFTVIOVLGMLGIAAGMKY 720
Db 661 FDHPNVTHLEGVYTKSPVMIITEFMENGSLDSFLRQNDGQFTVIOVLGMLGIAAGMKY 720
Qy 721 LADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDOTSDPTYSALGKFPRTWTAPE 780
Db 721 LADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDOTSDPTYSALGKFPRTWTAPE 780
Qy 781 AIOYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNDVINAIEODYRLPPMDCCPSALH 840
Db 781 AIOYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNDVINAIEODYRLPPMDCCPSALH 840
Qy 841 QLMIDCQOKDRNHRPKFGQIVNTLDKMIIRNPNSLKAMAPLSSGILNPLDRTIPDYTSFN 900
Db 841 QLMIDCQOKDRNHRPKFGQIVNTLDKMIIRNPNSLKAMAPLSSGILNPLDRTIPDYTSFN 900
Qy 901 TVDWMLEAIKMGQYKESFANAGFTSFVVSQMMMEDILRVGVTLAGHOKKILNSIOVMRA 960
Db 901 TVDWMLEAIKMGQYKESFANAGFTSFVVSQMMMEDILRVGVTLAGHOKKILNSIOVMRA 960
Qy 961 QMNOIOSVEV 970
Db 961 QMNOIOSVEV 970

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```

RESULT 4
US-08-542-635-2
Sequence 2, Application US/08542635
Patent No. 6218356
GENERAL INFORMATION:
APPLICANT: Pawson, Anthony
APPLICANT: Henkemeyer, Mark
APPLICANT: Letwin, Kenneth
TITLE OF INVENTION: NOVEL NEURAL RECEPTOR
TITLE OF INVENTION: TYROSINE KINASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr

```

STREET: 40 King Street West, Box 401
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/542,635
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: McDiarmid, Shona S.
 REGISTRATION NUMBER: 38,798
 REFERENCE/DOCKET NUMBER: 3153-162
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 TELEX: 06-23115
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 994 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Mus musculus
 DEVELOPMENTAL STAGE: Embryo
 IMMEDIATE SOURCE:
 LIBRARY: lambda gt10 cDNA library
 CLONE: Combined pNKRACE A2 and K2 and cDNA clones
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: Distal end of chromosome 4
 MAP POSITION: near the and-1 mutation
 US-08-542-635-2

Query Match 99.3%; Score 5082; DB 4; Length 994;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 1 ILAAVEETLMDSTTATAEIGWVHPSPGMEVSGYDENMNTIRTYQCVNVESSQNMWLR 60
 DB 23 ILAAVEETLMDSTTATAEIGWVHPSPGMEVSGYDENMNTIRTYQCVNVESSQNMWLR 82
 QY 61 TFEIRRGHRIHVHMKFSVRCSSIPVPGSKETFNLYYYEADFDSATKTFPMWENP 120
 DB 83 TFEIRRGHRIHVHMKFSVRCSSIPVPGSKETFNLYYYEADFDLATITFPMWENP 142
 QY 121 WKVVDTIADSEFSQVLDGGRVAKINTEVRSFGVSRSGFYLAFODYGCMSLIAVRFY 180
 DB 143 WKVVDTIADSEFSQVLDGGRVAKINTEVRSFGVSRSGFYLAFODYGCMSLIAVRFY 202
 QY 181 RKCPTIONGAIFQETLSAESTSLVAARGSCIANAEVDVPIKLYCGDGDWLPVIGRC 240
 DB 203 RKCPTIONGAIFQETLSAESTSLVAARGSCIANAEVDVPIKLYCGDGDWLPVIGRC 262
 QY 241 MCKAGEAVENTGVCRCGSGTFKANKOGDEACTHCPINSRTSSEGATNCVCNNGYRADL 300
 DB 263 MCKAGEAVENTGVCRCGSGTFKANKOGDEACTHCPINSRTSSEGATNCVCNNGYRADL 322
 QY 301 DPLDMCTTIPSAQAVISSVNETSLMEFWTPPRDSGGREDLYVNIICKSCSGGACACTR 360
 DB 323 DPLDMCTTIPSAQAVISSVNETSLMEFWTPPRDSGGREDLYVNIICKSCSGGACACTR 382
 QY 361 CGDNVYAPROGLTEPRYISDLAHTQYTFEIOAVNGVQSPSPFOFASVNTITNQA 420
 DB 383 CGDNVYAPROGLTEPRYISDLAHTQYTFEIOAVNGVQSPSPFOFASVNTITNQA 442

QY 421 APSAVSIMHOVSRTVDSITLTSMSQPDQPNGVIIIDYELQYVEKELESEYNATAIKSPNTVT 480
 DB 443 APSAVSIMHOVSRTVDSITLTSMSQPDQPNGVIIIDYELQYVEKELESEYNATAIKSPNTVT 502
 QY 481 -GLKAGAIYFQYARARTVAGYGRYSGRMVFQMTTEAEYQTSIOEKPLIIIGSSAGLVF 538
 DB 503 VQGLKAGAIYFQYARARTVAGYGRYSGRMVFQMTTEAEYQTSIOEKPLIIIGSSAGLVF 562
 QY 539 LIAVVIAIVCNRGRFERADESETDKQHTYTSGHITGKMTIYIDPFYEDPNEAVREFAK 598
 DB 563 LIAVVIAIVCNRGRFERADESETDKQHTYTSGHITGKMTIYIDPFYEDPNEAVREFAK 622
 QY 599 EIDISCVKIEOVYIGAGEFEGVCSGHLKPGKREIFVAIKTLKSGYTEKORRDFLEASIM 658
 DB 623 EIDISCVKIEOVYIGAGEFEGVCSGHLKPGKREIFVAIKTLKSGYTEKORRDFLEASIM 682
 QY 659 GQFDHPNVIHLEGVYTKSPVMIITEFMENGLSDSLRQNDGQTVYIQVGMRLGIAAGM 718
 DB 683 GQFDHPNVIHLEGVYTKSPVMIITEFMENGLSDSLRQNDGQTVYIQVGMRLGIAAGM 742
 QY 719 KTLADMNYYHRLAARNILVNSNLVCKYSDGLSFLFEDDTSDPTYSALGKPIRMFTA 778
 DB 743 KTLADMNYYHRLAARNILVNSNLVCKYSDGLSFLFEDDTSDPTYSALGKPIRMFTA 802
 QY 779 PEAIQYRKFTSADVKSQYGIYVMEVMSYGERPYMDTNOVYIMAEODYRLPPMDCPSA 838
 DB 803 PEAIQYRKFTSADVKSQYGIYVMEVMSYGERPYMDTNOVYIMAEODYRLPPMDCPSA 862
 QY 839 LHQMLDCQKORNHPRFGQIVNTLDKMRNPNSLKMAPLSSGINSPLDRTIPDVT 898
 DB 863 LHQMLDCQKORNHPRFGQIVNTLDKMRNPNSLKMAPLSSGINSPLDRTIPDVT 922
 QY 899 FNVVDMLFAIKMGQYKESFANAGFTSEPDVYSQMMEDILRVGVTLAHHOKKILINSIOM 958
 DB 923 FNVVDMLFAIKMGQYKESFANAGFTSEPDVYSQMMEDILRVGVTLAHHOKKILINSIOM 982
 QY 959 RAQMNQIOSVEV 970
 DB 983 RAQMNQIOSVEV 994

RESULT 5
 US-08-162-809-18
 ; Sequence 18, Application US/08162809
 ; Patent No. 5457048
 ; GENERAL INFORMATION:
 ; APPLICANT: Pasquale, Elena B.
 ; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: 4370 La Jolla Village Drive, Suite 700
 ; City: San Diego
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/162,809
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LJ 9503
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 995 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-162-809-18

Query Match 96.8%; Score 4950.5; DB 1; Length 995;
 Best Local Similarity 95.6%; Pred. No. 0;
 Matches 930; Conservative 28; Mismatches 12; Indels 3; Gaps 2;

QY 1 LLAAVEETLMDSTTATATLGMVHPSPGWEVSGYDENMNTIRTYOVQCNVFESSONMMLR 60
 DB 23 LLAAVEETLMDSTTATATLGMVHPSPGWEVSGYDENMNTIRTYOVQCNVFESSONMMLR 82
 QY 61 TKFTRRGARHRIHVEKMFVSDCSIPVSGCKETFNLYYEADPDSATKTFPMNMENP 120
 DB 83 TKYIRRGARHRIHVEKMFVSDCSIPVSGCKETFNLYYEADPDSATKTFPMNMENP 142
 QY 121 WVKVDITIADESFQVDLGGRYMKINTEVRSFGVRSRSGFYLAFODYGGCMLIAVRVY 180
 DB 143 WVKVDITIADESFQVDLGGRYMKINTEVRSFGVRSRSGFYLAFODYGGCMLIAVRVY 202
 QY 181 RKCPRIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDEMLVPIGRG 240
 DB 203 RKCPRIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDEMLVPIGRG 262
 QY 241 MCKAGFEAVENGTVCRGCPSTGTFKANOGEACHTCPINRSTTSEGATNCVCRNGYRDL 300
 DB 263 MCKAGFEAVENGTVCRGCPSTGTFKANOGEACHTCPINRSTTSEGATNCVCRNGYRDL 322
 QY 301 DPLDMOCTTPSPAPAVISSVNETSLMLEMTPRDSGREDLVYNIICKSCSGRGACTR 360
 DB 323 DPLDMOCTTPSPAPAVISSVNETSLMLEMTPRDSGREDLVYNIICKSCSGRGACTR 382
 QY 361 CGDNVQAPROLGLTEPRITRISDLAHTOYTFEIOAVNCTDOSPSPQAFANVTITNOA 420
 DB 383 CGDNVQAPROLGLTEPRITRISDLAHTOYTFEIOAVNCTDOSPSPQAFANVTITNOA 442
 QY 421 APSAVSIMQVSTVDSTLSWSODPQNGVILDYLOYYEKELSEYNATAIKSPNTVT 480
 DB 443 APSAVSIMQVSTVDSTLSWSODPQNGVILDYLOYYEKELSEYNATAIKSPNTVT 502
 QY 481 --GLKAGAIYFQVRRATVAGYGRSGKMYRQTMTEAEVQTSIQKLPILIGSSAAGLVF 538
 DB 503 YONLAKGTTIYVOVARATYAGTGRISGKMYRQTMTEAEVQTSIQKLPILIGSSAAGLVF 562
 QY 539 LLAVVYIAIVCN-RRGFERADSEVTDKLOHYTSGHITPGMKIYIDPFTYEDPNEAVREFA 597
 DB 563 LLAVVYIAIVCN-RRGFERADSEVTDKLOHYTSGHITPGMKIYIDPFTYEDPNEAVREFA 622
 QY 598 KEIDISCVIIEBOVIGAGEGVCCHLTKPKRRETFVAIKTKLSGYTEKQRDLSEASI 657
 DB 623 KEIDISCVIIEBOVIGAGEGVCCHLTKPKRRETFVAIKTKLSGYTEKQRDLSEASI 682
 QY 658 MGFDPHNVIIHLEGVYVSTPVMITTEFMENGSLDSFLRQNDGQFTYIQLVGMIRGTAAG 717
 DB 683 MGFDPHNVIIHLEGVYVSTPVMITTEFMENGSLDSFLRQNDGQFTYIQLVGMIRGTAAG 742
 QY 718 MKYLDMMYVIRDLAARILVNSMLVCVSPFGLSRLEDDTSDPYTYSALGKFPTRMT 777
 DB 743 MKYLDMMYVIRDLAARILVNSMLVCVSPFGLSRLEDDTSDPYTYSALGKFPTRMT 802
 QY 778 APEALQYRKFTSASDVMSYGIIVMEVMSYGERPYWDMTNDQVINAIDODVRLPPMPCPN 837
 DB 803 APEALQYRKFTSASDVMSYGIIVMEVMSYGERPYWDMTNDQVINAIDODVRLPPMPCPN 862
 QY 838 ALHQLMLDCKOKRNRHPRKFGQIYNTLDKMIARNPSLKAAPLSSGINFLPLDRTTIDYT 897
 DB 863 ALHQLMLDCKOKRNRHPRKFGQIYNTLDKMIARNPSLKAAPLSSGINFLPLDRTTIDYT 922

QY 898 SFNTVDEMLDAIKMQYKESFANAGFTSPDVYSOMMEDILRVGTLAGHOKKILNSIQV 957
 DB 923 SFNTVDEMLDAIKMQYKESFANAGFTSPDVYSOMMEDILRVGTLAGHOKKILNSIQV 982
 QY 958 MRAQNMQIOSVEY 970
 DB 983 MRAQNMQIOSVEY 995

RESULT 6

US-08-162-809-12
 Sequence 12, Application US/08162809
 Patent No. 5457048

GENERAL INFORMATION:

APPLICANT: Pasquale, Elena B.
 APPLICANT: Sajjad, Fereydoon G.
 TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:

ADDRESSEE: CAMPBELL AND FLORES
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California

COUNTRY: United States of America
 ZIP: 92122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/162,809
 FILING DATE:

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LJ 9503

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1011 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-162-809-12

Query Match 96.5%; Score 4934.5; DB 1; Length 1011;
 Best Local Similarity 94.0%; Pred. No. 0;
 Matches 930; Conservative 28; Mismatches 12; Indels 19; Gaps 3;

QY 1 LLAAVEETLMDSTTATATLGMVHPSPGWEVSGYDENMNTIRTYOVQCNVFESSONMMLR 60
 DB 23 LLAAVEETLMDSTTATATLGMVHPSPGWEVSGYDENMNTIRTYOVQCNVFESSONMMLR 82
 QY 61 TKFTRRGARHRIHVEKMFVSDCSIPVSGCKETFNLYYEADPDSATKTFPMNMENP 120
 DB 83 TKYIRRGARHRIHVEKMFVSDCSIPVSGCKETFNLYYEADPDSATKTFPMNMENP 142
 QY 121 WVKVDITIADESFQVDLGGRYMKINTEVRSFGVRSRSGFYLAFODYGGCMLIAVRVY 180
 DB 143 WVKVDITIADESFQVDLGGRYMKINTEVRSFGVRSRSGFYLAFODYGGCMLIAVRVY 202
 QY 181 RKCPRIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDEMLVPIGRG 240
 DB 203 RKCPRIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDEMLVPIGRG 262
 QY 241 MCKAGFEAVENGTVCRGCPSTGTFKANOGEACHTCPINRSTTSEGATNCVCRNGYRDL 300

MEDIUM TYPE: FLOPEY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/673.789
 FILING DATE:
 CLASSIFICATION: 4:5
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/177,812
 FILING DATE: 04-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: CAROL M. GRUPEL
 REGISTRATION NUMBER: 37,341
 REFERENCE/DOCKET NUMBER: 2026-4105
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 TELEX: 421792
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 995
 TYPE: AMINO ACID
 STRANDEDNESS: UNKNOWN
 TOPOLOGY: UNKNOWN
 US-08-673-789-5

```

Db 623 KEIDSCVKIIOVIGAGEFGEVCSGHLKLPCKREIFAIRTKLKGTYEKGRDPLSLASI 682
Qy 658 MGOEDHPNVHLLEGVYTKSTPYMITTEPMENGSLDSFLRNDQOFTYIOLVGLRGIAAG 717
Db 683 MGOEDHPNVHLLEGVYTKSTPYMITTEPMENGSLDSFLRNDQOFTYIOLVGLRGIAAG 742
Qy 718 MKYLADNMVYHRLDAARNILVNSNLVCKVSDFGLSRLEDDTSDPYTSALGSKFPLRMT 777
Db 743 MKYLADNMVYHRLDAARNILVNSNLVCKVSDFGLSRLEDDTSDPYTSALGSKFPLRMT 802
Qy 778 APEAIORRKTFSASDVWSYGIWMEVWSYGERPYWMTNODVYNAIEODYRLPPMDCPS 837
Db 803 APEAIORRKTFSASDVWSYGIWMEVWSYGERPYWMTNODVYNAIEODYRLPPMDCPN 862
Qy 838 ALHQLMDCQKORNRHPRKFGQIVNTLDKMIIRNPNSLKAMAPLSSGINLPDLDRTPDYT 897
Db 863 ALHQLMDCQKORNRHPRKFGQIVNTLDKMIIRNPNSLKAMAPLSSGINLPDLDRTPDYT 922
Qy 898 SFNTVDEMLAIKMGQYKESFANAGTSPEDVVSQMMEDILRAGVTYLAGHOKKILNSIOY 957
Db 923 SFNTVDEMLAIKMGQYKESFANAGTSPEDVVSQMMEDILRAGVTYLAGHOKKILNSIOY 982
Qy 958 MRAQNMQIOSVEY 970
Db 983 MRAQNMQIOSVEY 995

```

RESULT 8

US-08-673-789-6

Sequence 6, Application US/08673789

Patent No. 5814479

GENERAL INFORMATION:

APPLICANT: ZHOU, REMPING; SCHULZ, NICHOLAS,
APPLICANT: T. KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.

TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673, 789
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177, 812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 984
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN
US-08-673-789-6

Query Match 76.4%; Score 3909.5; DB 2; Length 984;
Best Local Similarity 73.9%; Pred. No. 1,7e-290;
Matches 716; Conservative 128; Mismatches 122; Indels 3; Gaps 2;

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Qy 2 LAABETLMDSTTAETAEELGMVHPSPGSEVSGYDENMNTTRTQOVONVNESSONMLRT 61
Db 15 VAAMEETLMDSTRITAEELGMVHPSPGSEVSGYDENMNTTRTQOVONVNESSONMLRT 74
Qy 62 KFIIRRGARHRIHVEKKSVDRCSSIPSPGCKETFLNYLYEADPDFSATKTFPMMEHP 121
Db 75 TFINRGARHRIHVEKKSVDRCSSIPSPGCKETFLNYLYEADPDFSATKTFPMMEHP 134
Qy 122 VKVDITADESFQVODLGGGRYMKINTEVRSGPRVSRGFLAODQGGSLAIVRYFR 181
Db 135 LKVDITADESFQVODLGGGRYMKINTEVRSGPRVSRGFLAODQGGSLAIVRYFR 194
Qy 182 KCPRIIONGAIPOETLSGAESTLVAARGSCIANAEEDVPILKLYCNGDGMVLPIGRCM 241
Db 195 KCPRIIONGAIPOETLSGAESTLVAARGSCIANAEEDVPILKLYCNGDGMVLPIGRCT 254
Qy 242 CKAGEAENGTVCRGCGPSTGFRKANGDEACTHCPIINSRTSGCATNCYCRNGYRADID 301
Db 255 CKAGEAENGTVCRGCGPSTGFRKANGDEACTHCPIINSRTSGCATNCYCRNGYRADID 313
Qy 302 PLDNPCTTIPSAPOAVISVNETSLMLEWPPRDSGREDLVYNIICKSGSGRGACTRC 361
Db 314 PPEVACTSVSPGRNVIISVNETSLMLEWPPRDSGREDLVYNIICKSGSGRGACTRC 373
Qy 362 GDNVQVAPROGLTERITISDLAHTOYFETIOAVNGVTDSPSPQASVNTITNOA 421
Db 374 DNVQVAPROGLTERITISDLAHTOYFETIOAVNGVTDSPSPQASVNTITNOA 433
Qy 422 PSAVSIHQVSRVDSITLSMSQDPOPGVNIIDYLOYEKELSEVMTAISPTNT--V 479
Db 434 PSTVPIHQVSRVDSITLSMSQDPOPGVNIIDYLOYEKELSEVMTAISPTNT--V 493
Qy 480 TGLKAGAIYFOVARTVAGYGRYSGMYFQMTAEVOTSIQERKLPLTIGSSAGLVFL 539
Db 494 DGLRPMGVYVOVARTVAGYGRYSGMYFQMTAEVOTSIQERKLPLTIGSSAGLVFL 553
Qy 540 IAAVVAIYCNRRGEFERADEYTDKLOHTSGHITTPGAKIYIDPTTYEDPNEAREFAKE 599
Db 554 VSLVAISIVCSKRAVSKAVYSDKLOHTSGHITTPGAKIYIDPTTYEDPNEAREFAKE 613
Qy 600 IDISCVKIEOVIGAGEFGEVCSGHLKLPCKREIFAIRTKLKGTYEKGRDPLSLASI 659
Db 614 IDISCVKIEOVIGAGEFGEVCSGHLKLPCKREIFAIRTKLKGTYEKGRDPLSLASI 673
Qy 660 OFDHPNVHLLEGVYTKSTPYMITTEPMENGSLDSFLRNDQOFTYIOLVGLRGIAAG 719
Db 674 OFDHPNVHLLEGVYTKSTPYMITTEPMENGSLDSFLRNDQOFTYIOLVGLRGIAAG 733
Qy 720 YLADNMVYHRLDAARNILVNSNLVCKVSDFGLSRLEDDTSDPYTSALGSKFPLRMT 779
Db 734 YLADNMVYHRLDAARNILVNSNLVCKVSDFGLSRLEDDTSDPYTSALGSKFPLRMT 793
Qy 780 EAIORRKTFSASDVWSYGIWMEVWSYGERPYWMTNODVYNAIEODYRLPPMDCPSAL 839
Db 794 EAIORRKTFSASDVWSYGIWMEVWSYGERPYWMTNODVYNAIEODYRLPPMDCPSAL 853
Qy 840 HQLMDCQKORNRHPRKFGQIVNTLDKMIIRNPNSLKAMAPLSSGINLPDLDRTPDYT 899
Db 854 HQLMDCQKORNRHPRKFGQIVNTLDKMIIRNPNSLKAMAPLSSGINLPDLDRTPDYT 913
Qy 900 NTVDENLEAIKMGQYKESFANAGTSPEDVVSQMMEDILRAGVTYLAGHOKKILNSIOY 959
Db 914 NTVDENLEAIKMGQYKESFANAGTSPEDVVSQMMEDILRAGVTYLAGHOKKILNSIOY 973
Qy 960 AQNMQIOSV 984

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Db 974 VQNMOSPSV 982

RESULT 9
US-08-162-809-2
Sequence 2, Application US/08162809

Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 951 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-809-2

Query Match 72.4%; Score 3706.5; DB 1; Length 951;
Best Local Similarity 70.2%; Pred. No. 5,2e-275;
Matches 687; Conservative 120; Mismatches 117; Indels 55; Gaps 4;

Db 7 ETIMDSTATAELGMMVHPGSGMEVSGYDDEMNTIRTYOVQCNVPESSONMLRTKFIIR 66
1 ETIMDSTATAELGMMVHPGSGMEVSGYDDEMNTIRTYOVQCNVPESSONMLRTKFIIR 60
67 RGAHRIHVMKFSVDCSSIPVSGCKETFNLYYEADFDSATKTFPNMKNENPVKVDY 126
61 RGAHRIHVMKFSVDCSSIPVSGCKETFNLYYEADFDSATKTFPNMKNENPVKVDY 120
127 IAADESFQVDLGRVMKINTVRSFGVSRSGFLAODYGGCMLAARVRYKCPRI 186
121 IAADESFQVDLGRVMKINTVRSFGVSRSGFLAODYGGCMLAARVRYKCPRI 147
187 IONGAIFQETLSGAEISTVAAAGSCIANAEVDPYIKLYCNGDEMLVPIGRCKAGF 246
148 VONFAIFPEITMGAEISTVAAAGSCIANAEVDPYIKLYCNGDEMLVPIGRCKAGF 207
247 EAVENGTVACGSGSTFKANQDEACTHCPINSRTSSEATNCVCNRYRADLPLDMP 306
208 EP-ENNACACAGAGTFFKASQAGLCARCPNRSASAEASPLACACNGYFRADLPLDMP 266
307 CTIIPSAQAVISSVNETSILEMTTPRDSGGEDLVYNIICKSSCGGACTRCGDNYO 366
267 CTSVPSGPRNVIVISVNETSILEMTTPRDSGGEDLVYNIICKSSCGGACTRCGDNYO 326

QY 367 YAPRODLTEPRYISDLAHOTYFEICQAVNGVTDSPOFASANTITNOAAPSAYS 426
Db 327 FVPRDLGTERFVSISSLMHAPTEICQAVNGVSNKSPFPPOHVSNTITNOAAPSAYS 386
QY 427 IMHOVSRTVDSITLSMSQPOPNVILDELYOYER-----ELSEY 467
Db 387 IMHOVSATMRISITLSMSQPOPNVILDELYOYER-----ELSEY 446
QY 468 NATAKSPNT-VTGLKACAIYFQVARTVAGYGVSGKMFOMTEAYOTSIOEKI 525
Db 447 NSSVARSQNTARLEGRPGVAVYQVARTVAGYGVSGKMFOMTEAYOTSIOEKI 506
QY 526 PLIGSSAGIVFLAVAVIAVNCNRRGFERADSEYDKLQHYTSGHITPGMKYIDPFT 585
Db 507 PLIGSSAGIVFLAVAVIAVNCNRRGFERADSEYDKLQHYTSGHITPGMKYIDPFT 566
QY 586 YEDPNEAVREPAKELISCVKIEOVIGAGEFVCSGHLKIPKRETFVAIKLKSQYE 645
Db 567 YEDPNEAVREPAKELISCVKIEOVIGAGEFVCSGHLKIPKRETFVAIKLKSQYE 626
QY 646 KORDFLSEASIMQFDHPNTHIEGVYTKSPVMTTEEMENGLSDPFLRNDGQFTVI 705
Db 627 KORDFLSEASIMQFDHPNTHIEGVYTKSPVMTTEEMENGLSDPFLRNDGQFTVI 686
QY 706 OLVMGMRGIAAGMKYIADNMYVHRDLAARNILVNSNLVCKVSDGLSRFLEDTSPTT 765
Db 687 OLVMGMRGIAAGMKYIADNMYVHRDLAARNILVNSNLVCKVSDGLSRFLEDTSPTT 746
QY 766 SAIGKFPRTAPVADYQKFTSASDVWSYGIWMEVMSYGERPYMONTODYINAEQ 825
Db 747 SSIIGKIPVMTAPVADYQKFTSASDVWSYGIWMEVMSYGERPYMONTODYINAEQ 806
QY 826 DYRLPPMPCPSALHOLMDCKQKRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSCIN 885
Db 807 DYRLPPMPCPSALHOLMDCKQKRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSCIN 866
QY 886 LPLDRTIPDYTSFNTVDEMLDAIKMGQYKESFANAGTSPDYVSQMMEDILRVGTLA 945
Db 867 QPLDRSIPDYTSFNTVDEMLDAIKMGQYKESFANAGTSPDYVSQMMEDILRVGTLA 926
QY 946 GHOKTILNSIQVMKVMQ 964
Db 927 GHOKTILNSIQVMKVMQ 945

RESULT 10
US-08-162-809-10
Sequence 10, Application US/08162809
Patent No. 5457048

GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

196 TISGASTSLVARGSCINAEVDVPIKXCNQDGEMLVPIGRCKAKGAEVANGTVC 255
197 TITGAPETSLVAPGTCINAEVSVPLKLYCGDEMMVPGACGACGAYEPAMKDTQC 256
256 RCPSTFFANQDEACTHCPIINSRTSGATNCVCRNGYRRADLDPLMPCPTTISAQ 315
257 QACGPETFSKQGECCSCPCPSRRTAGAAVYCICRSQGFRRADADPADSACTSVSAR 316
316 AVISSVNETSLMEWTPPRDSGGREDLVYNIICKSCSGRACRGTGCDNVQVAPRL--- 372
317 SVISNNETSLVLEWSEPDAGGRDLDLVNICKCSVRRLCSRDDNVEFPRLGLT 376
373 GLTEPRITSLIAHQYFEIOAVNGVDSPPSPFASVNTTQAAPSAHSIMHOVS 432
377 GLTERITYSKVAHPQYFEIOAVNGISSKSTPPHPSVNTTQAAPSAHPHLLHS 436
433 RYVDSITLSMSPDPDNGVILDELOYEKE--LSEYNATAIKSPNTV--TGKACAIVY 489
437 STGNSMTLSMTPEPENGILDEYIKSEKQGGDIANTVYSQKNSVRLDGLKANARYM 496
490 FOVRANTVAGYGRYSKMTFQMTAEYOTSTOEKPLIIGSSAAGLVELIANVYAIYC 549
497 VOVRANTVAGYGRYSLPTFEOTAEDEGSKTFQELPLIVGSATAGLEIVIVVIAIYC 556
550 NRRGF-----ERADSEYTDKLOHYTSGHITPGKXIYIDPPTYEDPNEAYR 594
557 FRKGMVTEOLLSPGLRKQNSNDPPEYTEKLOQ---VTPGKXIYIDPPTYEDPNEAYR 612
595 EFAKEIDISCVKIEOYIGAGEFEVCSGHLKLPGRKEIFAIAKTLKSGYTEKORDFLE 654
613 EFAKEIDISCVKIEEYIGAGEFEVCSGRGLKLPGRKEIFAIAKTLKSGYTEKORDFLE 672
655 ASIMGCFDHPNVIHLEGVYTKSTPVMITTEFMENGLSDFLRNDQGFYIOLVGMIRGI 714
673 ASIMGCFDHPNVIHLEGVYTKSRPMITTEFMENCALDFLRNDQGFYIOLVGMIRGI 732
715 AAGMKTLAMNHYHRLAARNILVNSNLVCYKVSDFLSRLEDDTDPYTSALGSKFPI 774
733 AAGMKTLSENNYHRLAARNILVNSNLVCYKVSDFLSRLEDDTDPYTSALGSKFPI 792
775 RMTAPAIQYRKFTSASDVWSYGVIMVEWVSGERPYMDTNDVINAIEODYRLPPMD 834
793 RMTAPAIYRKFTSASDVWSYGVIMVEWVSGERPYMDSNODVINAEODYRLPPMD 852
835 CPBALHQLMLDCQKRNHRPKGOIVNLDKIRMPNSLKAAAPLSSGINPLDRLTIP 894
853 CPBALHQLMLDCQKRNHRPKGOIVNLDKIRNAASLKVTASVQSGVSLDRLTIP 912
895 DYSFNTVDEMLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRAGVTLAGHOKILNS 954
913 DYTFTTVDMDLAIKMGYKESFANAGFTSPDVVSQMMEDILRAGVTLAGHOKILNS 972
955 IOVRAQMOQIOSVEY 970
973 IODMRLQMOQLPEVQY 988

RESULT 12
US-08-449-645A-20
Sequence 20, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF INVENTIONS: 43
TITLE OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBM
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: A:5
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-20

Query Match 71.0%; Score 3632.5; DB 2; Length 998;
Best Local Similarity 70.5%; Pred. No. 2.6e-269;
Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

4 AVEETLMDSTTAEIAGMNVHPSPGWEVSGYDENNTIRTYOVGVNPESSONMLRTKE 63
1 AVEETLMDSTTAEIAGMNVHPSPGWEVSGYDENNTIRTYOVGVNPESSONMLRTKE 63
37 ALEETLMDKWTSETLAWSHSPESGEVSGYDEANPRTYQVNCVRRSSONMLRTKE 96
64 IRRGARHIVHEKFEIVRCCSIPSVGCKETFNLYYEADFDSATKTPPMNMNVK 123
97 IMRDQYRYVELKFTVYRONSIPNIGCKETFNLFYEADSDVASASSPMMENPVYK 156
124 VDTIADESPQYDLCGRYKINTVEYRSPVRSRGTAFODYGGCMGLIARVYRKC 183
157 VDTIADESPQYDLCGRYKINTVEYRSPVRSRGTAFODYGGCMGLIARVYRKC 212
184 PRIOGALFOETLSGAEASTSLVARGSCINAEVDVPIKXCNQDGEMLVPIGRCKM 243
213 ASTTAGFALPELTGAEFTSLVIAFGTCIPNAVEYSVLKLYCNDGEMMVPVGACTA 272
244 AGEAEVANGTVCRCGSGTFKANQGDCACTHCPINSRTSGATNCVCRNGYRRADLDPL 303
273 TGEHPAAKSKQCRCPGSGYKAKQGECPCLPCPNSRTTSPAASICTCHNFEYRADSDA 332
304 DMECTTIPAPQAVISVNETSLMEWTPPRDSGGREDLVYNIICKSC--GSGRACRGC 361
333 DSACTVPPSPRGVYINNETSLILEWSEPRDGVGRDLDLVNICKCSGAGAGASCSRC 392
362 GDNVOYAPROLGLTERIRYISDLAHTOYFETIOAVNGVDSPPSPFASVNTTQAA 421
393 DDNVEFPROLGLTERIRYISDLAHTOYFETIOAVNGVDSPPSPFASVNTTQAA 452
422 PSASVIMHOVSRTVDSITLSMSPDPDNGVILDELOYEKEKELSEYNATAIKSPNTV-- 479
453 PSEVPTRLRHSSSGSILTSMAPPERNGVILDEYEMKYEK--SEGIASTVTSQMSVOL 510
480 TGKACAIVFOVRANTVAGYGRYSKMTFQMTAEYOTSTOEKPLIIGSSAAGLVAF 538
511 DGLRPARYVOVRANTVAGYGRYSKMTFQMTAEYOTSTOEKPLIIGSSAAGLVAF 570
539 LIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHITPGKXIYIDPPTYEDPNEAREFAK 598
571 VAANVIAIVCLRKQHGSDSETTEKLOQ---IAPGKXIYIDPPTYEDPNEAREFAK 626
599 EIDISCVKIEOYIGAGEFEVCSGHLKLPGRKEIFAIAKTLKSGYTEKORDFLSASIM 658
627 EIDVSCVKIEEYIGAGEFEVCSGHLKLPGRKEIFAIAKTLKSGYTEKORDFLSASIM 686
659 GQFDHNVHLEGVYTKSTPVMITTEFMENGLSDFLRNDQGFYIOLVGMIRGI 718
687 GQFDHNVHLEGVYTKSTPVMITTEFMENCALDFLRNDQGFYIOLVGMIRGI 746

QY 719 KYLADNMYVHRDLAARNILVNSMLYCKVSDGSLRFLLEDTSOPITYSALGCKFPIRMWA 778
 DB 747 KYLENNYVHRDLAARNILVNSMLYCKVSDGSLRFLLEDTSOPITYSALGCKFPIRMWA 806
 QY 779 PEAIORRKTFTSASDVMSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLRPPMDCPSA 838
 DB 807 PEAIARKTFTSASDVMSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLRPPMDCPSA 866
 QY 839 LHQMLDCKMOKDRNRHPRKFGQIVNTLDKMIIRNPNSLKAMAPLSSGINTLPLDRTPIDYTS 898
 DB 867 LHQMLDCKMOKDRNRHPRKFGQIVNTLDKMIIRNPNSLKAMAPLSSGINTLPLDRTPIDYTS 926
 QY 899 FNTVDMLAIIKMGQYKESFANAGFTSPDVVSOMMEDILRVGVTLLAGHOKKILNSIQVM 958
 DB 927 FTTVGMDLAIKMGKRYKESFVSGFASFDLVQAQMTAEDLLRIGVTLAGHOKKILNSIQVM 986
 QY 959 RAQMNQIOSEV 970
 DB 987 RLQMNQTLPOV 998

RESULT 13

US-08-702-367A-20
 ; Sequence 20, Application US/08702367A
 ; Patent No. 5981246
 ; GENERAL INFORMATION:
 ; APPLICANT: Fox, Gary M.
 ; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
 ; TITLE OF INVENTION: Kinases
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Patent Operations/RBW
 ; STREET: 1840 Dehaven Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 91320
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/702.367A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Winters, Robert B.
 ; REFERENCE/DOCKET NUMBER: A-287
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 998 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-702-367A-20

Query Match 71.0%; Score 3632.5; DB 2; Length 998;
 Best Local Similarity 70.5%; Pred. No. 2.6e-269;
 Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

QY 4 AVEETLMDSTTAETALGMLVHPSPGMEVSGYDENMNTIRTYQVCNVESSQNMMLRTKF 63
 DB 37 ALBETLMDTKVTSSELAVTSPGMEVSGYDENMNTIRTYQVCNVESSQNMMLRTKF 96
 QY 64 IRRGARRIHVEKFSVSDSSISVSGCKETNLYYEADPFSAKTKTPNNKNEPWAK 123
 DB 97 IWRDVOVRYVELKFTYVDCSINIPGSCETNLYYEADPFSVASSSPFMMENPVYK 156
 QY 124 VDTIADESFSQVLDGGRVKNINTEVRSFGVFLAFQDYGGCMSLIAVAVFRKC 183

DB 157 VDTIAPDESFSRLDAG----RYNTRVRSFGPLSKAGFLAQQDQACMSLISVAFRYKCK 212
 QY 164 PRILONGALFOETLSGASTSLSVAARGSCIANAEVDPYILYCGDGEWLPIGRCKCK 243
 DB 213 ASTTAGLFPETTLTGABPTSLVIAPGTCIPNAVEVSPKLYLCNGDGEWMPVAGACTCA 272
 QY 244 AGFEAVENGTCRCGPSTPFANOGDEACTHCIPINSRTSGATNCVRCNYTRADLDPL 303
 DB 273 TGHETAAEESQCRCPSPSTYAKQGEPCLPSPKRTSPAAISCTCHNHFYRADSDSA 332
 QY 304 DMPCTTISAPQAVISSVNETSLMLEWTPPRDSGREDLVNIITCKSC--GSGRAGACTRC 361
 DB 333 DSACTTVPSPRGVSNVNETSLILEMSEPRDLGVRODLYLVNICKCHGAGASASRC 392
 QY 362 GDNQYARROGLTEPRITIDLAHQYTTEIQAVNGVTDQSPSPQFASVNTITNOAA 421
 DB 393 DDNEFVPRQLGSEPRVHTSHLAHRTYTEVQAVNGVSGKSPUPRYAAVNITITNOAA 452
 QY 422 PSASIMHQVSRVDSITLSNSOPDOPNGVILDEYELQYERKELSEYNATAIKSPNTNV-- 479
 DB 453 PSEVPTLRHSSSGSLTSMAPPERNGVILDEYEMKTEF--SEGIASTVTSQMSVOL 510
 QY 480 TGLAAGAIYVQVARTVAGYGRYSGMYFQMTA--AEYOTSIOEKLPLIIGSSAGLVF 538
 DB 511 DGLRPDARYVQVARTVAGYGRYSGMYFQMTA--AEYOTSIOEKLPLIIGSSAGLVF 570
 QY 539 LIAVVAIVAVNRRGFERADSEYTDKLOHTYSHGITGKMTIYDPPEYEDNEAVREFAK 598
 DB 571 VVAVVAIVAVNRRGFERADSEYTDKLOHTYSHGITGKMTIYDPPEYEDNEAVREFAK 626
 QY 599 EIDISCVKIEQVIGAGEGEGVSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLEASIM 658
 DB 627 EIDVSCVKEIEVIGAGEGEGVSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLEASIM 686
 QY 659 GQDPHPVTHLEGVYVSTPYMITTEFMENGLSDSFLRQNDGQFTVQLVGMRLGIAGM 718
 DB 687 GQDPHPVTHLEGVYVSTPYMITTEFMENGLSDSFLRQNDGQFTVQLVGMRLGIAGM 746
 QY 719 KYLADNMYVHRDLAARNILVNSMLYCKVSDGSLRFLLEDTSOPITYSALGCKFPIRMWA 778
 DB 747 KYLENNYVHRDLAARNILVNSMLYCKVSDGSLRFLLEDTSOPITYSALGCKFPIRMWA 806
 QY 779 PEAIORRKTFTSASDVMSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLRPPMDCPSA 838
 DB 807 PEAIARKTFTSASDVMSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLRPPMDCPSA 866
 QY 839 LHQMLDCKMOKDRNRHPRKFGQIVNTLDKMIIRNPNSLKAMAPLSSGINTLPLDRTPIDYTS 898
 DB 867 LHQMLDCKMOKDRNRHPRKFGQIVNTLDKMIIRNPNSLKAMAPLSSGINTLPLDRTPIDYTS 926
 QY 899 FNTVDMLAIIKMGQYKESFANAGFTSPDVVSOMMEDILRVGVTLLAGHOKKILNSIQVM 958
 DB 927 FTTVGMDLAIKMGKRYKESFVSGFASFDLVQAQMTAEDLLRIGVTLAGHOKKILNSIQVM 986
 QY 959 RAQMNQIOSEV 970
 DB 987 RLQMNQTLPOV 998

RESULT 14

PCT-US95-04681-20
 ; Sequence 20, Application PC/TUS9504681
 ; GENERAL INFORMATION:
 ; APPLICANT: Fox, Gary M.
 ; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
 ; TITLE OF INVENTION: Kinases
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Patent Operations/RBW
 ; STREET: 1840 Dehaven Drive
 ; CITY: Thousand Oaks
 ; STATE: California

Query Match	71.0%;	Score 3632.5;	DB 5;	Length 998;
Best Local Similarity	70.5%;	Pred. No. 2.6e-269;		
Matches 685;	Conservative 114;	Mismatches 158;	Indels 15;	Gaps 6

Db	687	GOFHPNITILEGVVTSRPMILITEMENALDSFLRLNDGGFTVILQGLMRLGIACM	746
Qy	719	KYLADMNVVHDDLAEFNILVNSNLVCXVSDFGLSRFLEDDTSDEPTYTSAIGKFPIMTA	778
Db	747	KYLSMNNVHSDLLAEFNILVNSNLVCXVSDFGLSRFLEDDPSDEPTYTSLGKKIPIMTA	806
Qy	779	PEALDYKRFETASVWSVSGIYMMVEVMSGEPBPYDMNODIYNALIEDDYRLPMPDPCSA	838
Db	807	PEALAYKRFETASVWSVSGIYMMVEVMSGEPBPYDMSNODYINAVEDDYRLPMPDPCPTA	866
Qy	839	LHQLMLDWCOKDRHHEPKFGQIVNTLDMKIRNPNSLKMAMPSSGIMLPLDRTIPDYS	898
Db	867	LHQMLDWCWVADRNLHPFESQIVNTLDTLKLIRNAASLKVIVASQSGMSQPLDRTVPDYTT	926
Qy	899	FNIVDEWLEAIKMCQYKESFANAGFTSPDYVSOMMEDILRVGTYTLAGHOKKILINSIQVM	958
Db	927	FTTVQDMIDLAIKMGYKESFVSASFASFDLVAOMTAEIDLRIIGVTLAGHOKKILISTIQDM	966
Qy	959	RAQNMQIQSVVEY 970	
Db	987	RLQNMQITLPCVQ 998	

RESULT 15
 US-08-673-789-7
 : Sequence 7, Application US/08673789
 : Patent No. 5614479
 : GENERAL INFORMATION:
 : APPLICANT: ZHOU, REMPING; SCHULZ, NICHOLAS,
 : APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
 : APPLICANT: GEORGE, P.
 : TITLE OF INVENTION: BSK RECEPTOR LIKE
 : TITLE OF INVENTION: TYROSINE KINASE AND THEIR
 : TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
 : TITLE OF INVENTION: METHODS
 : NUMBER OF SEQUENCES: 14
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: MORGAN & FINNEGAN
 : STREET: 345 PARK AVENUE
 : CITY: NEW YORK
 : STATE: NEW YORK
 : COUNTRY: USA
 : ZIP: 10154
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: FLOPPY DISK
 : COMPUTER: IBM PC COMPATIBLE
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WORDPERFECT 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/673,789
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/177,812
 : FILING DATE: 04-JAN-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: CAROL M. GRUPE
 : REGISTRATION NUMBER: 37,341
 : REFERENCE/DOCKET NUMBER: 2026-4105
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 758-4800
 : TELEFAX: (212) 751-6849
 : TELEX: 421792
 : INFORMATION FOR SEQ ID NO: 7:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 970
 : TYPE: AMINO ACID
 : STRANDEDNESS: UNKNOWN
 : TOPOLOGY: UNKNOWN
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Query Match	70.3%	Score 3595.5	DB 4	Length 970
Best Local Similarity	70.0%	Pred. No. 1,6e-266		
Matches 671	Conservative 115	Mismatches 161	Indels 11	Gaps 4
OY	16	TALGMAVHPSPGMEVSVGYDENMNTIRTYQVCNVFESSQNNMLARTKRIIRCAHIIHVE	75	
Db	21	TSEIATMTHTBETGMEVSVGYDEAMOPIRTYQVCVREAOQQMLRKRTKFINRQDVQRYVE	80	
OY	76	MKFEVRCCSSIPSPGCKETENLYYEADFDSATITPPMBENPVKVDITLADESFO	135	
Db	81	LKFTVRCRCKIPIPIGSKETENLIFYESTSDSASNSPMENPNKIKDTIAPDESFSK	140	
OY	136	VDLGVMKINTEEVRSFGVPSRSGFYLAOFDYGGCSLILAVRFYKCPRIIONGAIPE	195	
Db	141	LESG---RVNTKYRSFGPLSKNGFYLAODIGACMSLILVAFYKCSNTIAGRAIPE	196	
OY	196	TLSGAESTSLVAARGSCINAAEVDVPIILYKCGDEMLVPIGRCKMCKAFEAVENTVC	255	
Db	197	TLTGAETSLVLAAPGCIIPQAAEVSPILLYKCGDEEMVVPVAGACTCAAGYEPAPKDTQC	256	
OY	256	RGPSPGTFRANOGDEACTHCPIINSRTSGATNCVGRNGYVRADIDPDIPTTIPSAPO	315	
Db	257	QACGPPTFSKQEGEPCPCPPSRSTTAAATVCIICRSGFPFADPADPSACTSVSAPR	316	
OY	316	AVTSSVNETSLMEVTPPDSDGREDLVNIITCKSGSGRACGTRCGDNOYVAPRQLLT	375	
Db	317	SVTSSVNETSPLEWSEPDAGGRDOLLVNIITCKCSVERILCSGCDNVEVFPRQLLT	376	
OY	376	EPRIYISDLATQYTFEELQAVNGVLYDPSFPQASVITITNOAASVSIIMHOVSTV	435	
Db	377	ERRITYSKVMAHPQYTFEIOAVNGVSISSKSPYRPHRASVITITNOAVLSAVPMLHSTG	436	
OY	436	DSLTSSQSPDPDNGVILDYELQYIEKE--LSTYNATAIKSPNTV--TGLAGAIYVRQV	492	
Db	437	NSMTLSMTPEPENGILIDYELIKYSEKQGGGINTYTSOKNSVRDLGKANARVYQV	496	
OY	493	RARTVAGYGRYSKMYPQTMTEAEYQTSIOEKLPIITISSAAGLFLTAVVAVIYVCR	552	
Db	497	RARTVAGYGRYSLPEFQYTAEDGSTKTPQELPLIVGSAAGLFLVIVVITAIYVCRK	556	
OY	553	GFERADSEKTDLOHYTSGHITPGKIIYIDPPTYEDPNAVREPAKETIDISCVKIEOYIG	612	
Db	557	QANSNDPEYTEKLOOY---VTPGKKIYIDPPTYEDPNAVREPAKETIDISCVKIEEYTG	612	
OY	613	AGEFEVCSGLHLRPGKREIFAVALTKLTSGETEKORRDFLSEASIMQFDPHPNIHIEGV	672	
Db	613	AGEFEVCRGLKLTPGKREIFAVALTKLVGYTERORRDFLSEASIMQFDPHPNIHIEGV	672	
OY	673	VKSPVMIITPEFMNGSLDPSLRNDQOFVIOUYGLRILIAAGKTYLADMTVVRDOLA	732	
Db	673	VTKSPVMIITPEFMNGSLDPSLRNDQOFVIOUYGLRILIAAGKTYLSEMTNVHRDOLA	732	
OY	733	ARNILVNSNLVCKVSDFGLSRFLDDTSDPTTYTALGGKFPRIINTAREALIOYRKFTSASD	792	
Db	733	ARNILVNSNLVCKVSDFGLSRFLDDPADPPTYTSLGKIPRIINTAREALIAKFTSASD	792	
OY	793	VWSYGVIVMVEWVSGERPYMTNODVYINALEOYRILPPPHDCSALHQLMDQWQKDRN	852	
Db	793	VWSYGVIVMVEWVSGERPYMTNODVYINAEQYRILPPPHDCJTAHQLMDQWQKDRN	852	
OY	853	HRPFGQIVNTLDMKIRNPNSLKAAPLSGGINPLDRTIPDTSFNTDEWLEAIKMG	912	
Db	853	LRPKRAQIVNTLDMKIRNPNSLKAAPLSGGINPLDRTIPDTSFNTDEWLEAIKMG	912	
OY	913	QKSEFAVAGCTSPDYVSOMMEDILVGVYGLGHOKKILNSIQVRAQONQIQSEV	970	
Db	913	RYKENFVHHGASDVLQAKMTAEIDLIGVYGLGHOKKILNSIQVRAQONQIQSEV	970	

Search completed: July 24, 2001, 16:29:09
Job time: 345 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2001, 16:21:49 ; Search time 24.02 Seconds

(without alignments)
2448.179 Million cell updates/sec

Title: us-09-378-759-11

Sequence: 1 LLAIVETLMDSSTATATLGL.....ILNSIQVMRAQNMQISVEV 970

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5116	100.0	970	AA85089	Eph-like receptor
2	5092	99.5	1055	AA819591	Human CASB616
3	5082.5	99.3	987	AA819590	Human CASB616
4	5082	99.3	994	AAW26366	Mouse Nuk tyrosine
5	5078	99.3	994	AA887018	Receptor tyrosine
6	4950.8	96.8	995	AA875712	Eph-related PTK Ce
7	4834.5	96.5	1011	AA875709	Eph-related PTK Ce
8	3806.5	76.4	984	AA844513	elk. Rattus rattu
9	3698.5	72.3	951	AA875704	Eph-related PTK Ce
10	3656	71.5	973	AA875708	Eph-related PTK Ce
11	3649.5	71.3	988	AA875710	Eph-related PTK Ce

12	3622.5	70.8	990	AA81899	Human embryonal K1
13	3590.5	70.2	993	AA875843	Protein p140 CDNA
14	3590.5	70.2	993	AA875844	Protein p140 CDNA
15	3326.5	65.0	973	AA875707	Eph-related PTK Ce
16	3031	59.2	986	AA885091	Eph-like receptor
17	3031	59.2	991	AA885090	Eph-like receptor
18	3024	59.1	986	AA885092	Eph-like receptor
19	3016	59.0	998	AA885092	Eph-like receptor
20	3001	58.7	998	AA885092	Eph-like receptor
21	2918.5	57.0	983	AA808665	Mouse developmenta
22	2917.5	57.0	983	AA808665	Mouse developmenta
23	2910	56.9	983	AA875711	Amino acid sequenc
24	2907	56.8	1005	AA883147	A human EphA5 HLA
25	2889.5	56.5	983	AA83146	Eph-related PTK Ce
26	2827.5	55.3	987	AA889263	Rat receptor tyros
27	2827.5	55.3	987	AA889263	Human non-differen
28	2827.5	55.3	987	AA889263	Protein tyrosine-k
29	2827.5	55.3	987	AA889263	Full length recept
30	2825.5	55.2	987	AA894652	Receptor type tyro
31	2816.5	55.1	972	AA876468	Receptor type tyro
32	2816.5	55.1	972	AA876468	Mature non-differe
33	2780.5	54.3	1293	AA841896	PTK gene HPRK5 pro
34	2714.5	53.1	849	AA875706	Eph-related PTK Ce
35	2611.5	51.0	928	AA87853	Rat REK7 eph-relat
36	2600	50.8	948	AA883148	Rat receptor tyros
37	2442	47.7	877	AAW71628	Mouse Bsk receptor
38	2439	47.7	1006	AAW70525	Human thymus recep
39	2439	47.7	1021	AAW70526	Human thymus recep
40	2438	47.7	1006	AAW72256	Human thymus recep
41	2256	44.1	722	AA875705	Eph-related PTK Ce
42	2238	43.7	744	AA875713	Eph-related PTK Ce
43	2167	42.4	710	AA875714	Eph-related PTK Ce
44	1951.5	38.1	856	AA827656	Human protein PRO3
45	1871.5	36.6	977	AAW19258	Embryonic stem cel

ALIGNMENTS

```

RESULT 1
ID AAR85089 standard; Protein: 970 AA.
AC AAR85089;
DE 16-APR-1996 (first entry)
Eph-like receptor protein tyrosine kinase HEK5.
KW Eph-like receptor protein tyrosine kinase; PTK; HEK5;
KW human eph-like kinase; therapy; diagnosis; vector; antibody.
OS Homo sapiens.
PN WO9528484-A1.
PD 26-OCT-1995.
PF 14-APR-1995; 95WO-US04681.
PR 15-APR-1994; 94US-0229509.
PA (AMGE-) AMGEN INC.
PI Fox GM, Jing S, Welcher AA;
XX WPI: 1995-373799/48.
XX N-PSDB: AAT02946.
XX
XX New nucleic acid encoding Eph-like receptor tyrosine kinase(s) -
XX and related vectors, host cells, proteins, antibodies etc., used
XX diagnostically and therapeutically to modulate receptor activation
XX or prodn.
PT

```


Query Match 99.58; Score 5092; DB 21; Length 1055;
 Best Local Similarity 99.68; Pred. No. 0;
 Matches 967; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

1 LLAAVEETLMOSTTATATAGMNVHPPSGWEVSGVDENMNTTRTYOVGVFSSQNNMLR 60
 15 llaaveetlmosttataetlaelgmwvhpssgweevsgydenmnltrtygvcnvfessqnnmlr 74
 61 TKFIRRGAGRHLHVMKFSVDCSSIPSPSCKETENFLYYEADFDSATKTFPMNMENP 120
 75 TKFIRRGAGRHLHVMKFSVDCSSIPSPSCKETENFLYYEADFDSATKTFPMNMENP 134
 121 WVKVDTTADSFQVLDGGMKINTEVRSFGVSRSGFLAFODYGGCNSLIARVRY 180
 135 wkvvdtlaadefsqvldggrvmkintevrsfgvrsrgfylafoayggcnsliarvry 194
 181 RKCPRIIONGAIPOETTSAGSTSLVAAAGSCIANAEVDVDPITLXNCGDCEMLVPTRGRC 240
 195 rkcpriiongaipogttsagstslvaagscianaevdvdpitlxncgdcemlvprgrc 254
 241 MCKAGFEAVENGTVCRGCPSCGTFKANOGEDEACTHCPINSRTTSGATNCVCRNGYRADL 300
 255 mckagfeavengtvcrpgscgtfkangodeacthcnpsrttsgatncvcrngyradl 314
 301 DPLMPCTTISARQAVISSNETSLMEWTPPDSCGREDLVYNIICKSCSGRGACTR 360
 315 dplmpcttisarpqvissnetslmewtppdscgredlvyniickscsgrgactr 374
 361 CGDNVQYAPRQGLTERPRIVTSDLAHTQYTFEIOAVNGVTDSPSPFOPFASVNTTNOA 420
 375 cgdnvqyaprqglterpriysdlahtqytfelqavngvtdspspfpofasvnttnoa 434
 421 APSAVSIHMOVSRTVDSITLWSQPDQPNVILDELOVEKESEYNATAIKSPNTVT 480
 435 apsavsihmovsrtvdsitlwsqpdqpnvildelovekeseynataikspntvt 494
 481 - -GLKAGAIYFOVRAFTVAGCYGRYSKMYFQYTFEAETQSTIOEKPLIIGSSAGLVF 538
 495 vqgikagailvfovravftvagcygryskmyfqteteeaytsiqekplilgssaglvf 554
 539 LIAVVVAIYCNRRGFEPRADSEYTDKLOHTSGHITPGMKIYIDPPYEDPNEAVREFAK 598
 555 liavvvaitycnrrgfepradseytdklohtsghtpgmkityidppyedpneavrefak 614
 599 EIDISCVKIQVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORRDELSASIM 658
 615 eidiscvkiqvigagefgevcsghlkpgkreifvaliklksagytekordelsasim 674
 659 GOFHPRVHILEGVVTKSTVMTITERMENGSLDSFLRONDGQFTVQLVGMRLGTAAGM 718
 675 gofhprvhilegvvtskstvmtitermengslsflrondgqftvqlvgmrlgtaagm 734
 719 KYLADNMYVRDLAARILVNSNLVCVSPDFGLSRFLEDSTDPPTYSAIGKFEPIRWTA 778
 735 kyladnmyvrldlaarilvnsnlvcvspdfglstrfledstdpptysaigkfeplrta 794
 779 PEALQYRKFTSASDVSYGIVMEVWSYGRPYWDMTNDVINAIEODYRLPPMDCPSA 838
 795 pealqyrkftsasdvsygivmewwsygrpywdmtndvinaieodyrlppmdcpsa 854
 839 LHLMLDCKMOKDNHRPKFGQIYNTLDKMTIRNNSLKAAAPLSSGINPLLDRTTIDYTS 898
 855 lhlmldckmoxdnhrpkfgqiyntldkmtirnpnslkamaplssginplldrttdyts 914
 899 FNTVDEMLKIKGOYKESFANAGFTSFVVSQMMMEDILRVGVTLAGHOKITLNSIOVM 958
 915 fntvdeamlkikgoykessfanagftsfvvsqmmmedilrvvgvtlaghokitlnsiom 974
 959 RAQMNOIQSVE 969
 975 raqmnoiqsve 985

RESULT 3
 AAB19590
 ID AAB19590 standard; Protein; 987 AA.

XX AC AAB19590;

XX DT 22-JAN-2001 (first entry)

XX DE Human CASB616.

XX KW CASB616; EPHB2; ERK; EPH3; EPH3; DRT; HEK5; EPHB2v;

XX KW receptor protein tyrosine kinase; human; antigen; colon cancer;

XX KW ovary cancer; tumour; autoimmune disease; vaccine; therapy;

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

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FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

FT FT MISC-difference 568..569 /note="an additional Arg residue decodes from the

```

OY 61 TFEIRRRGARHRIHVENKESVSDCCSIPSVGCKETFNLYYEADFDASVTKTPEPMNEMP 120
    |||||||
DB 75 kffirrrghrhlhvemkfvdrccsipsvgcketfnlyyeadfdsatcklfpmwemp 134
    |||||||
OY 121 WKVVDTIADSEFSQVLDGRVWKINTFVRSRGPVRSRGFTYLAFOYGGCMSLIARVRY 180
    |||||||
DB 135 wkvvdtaadesfsqvdlygrvwmkntevrsfgrvrsqfylafoqyggcmsliavrly 194
    |||||||
OY 181 RKCPRITONGAIFQETLSGAESTSLVAANGSCIANAEVDVPIKTCNCGEMLVPIGRC 240
    |||||||
DB 195 rkcpriingalfqetlsgaestsivaargscianaeevdpiklycngdgemlvpiygrc 254
    |||||||
OY 241 MCKAGFEAVENGTVCRGCPSTFKANQGDACHCPINRRTTSEGATNCVCNRRYRDL 300
    |||||||
DB 255 mckagfeavengtvcrpcpsgtfkangdeachcpinsrttsegatncvcnryyrdl 314
    |||||||
OY 301 DPLDMCCTTIPSPAPAVISVNETSLMELMTPPRDSGREDLYNNTICKSCSGRGACATR 360
    |||||||
DB 315 dpldmcccttspapavisvnetslmlewtpprdsgrredlynnlickscsgsgrgacatr 374
    |||||||
OY 361 CGDNVOYAPROLOTEPRIRIYISDLAHTQYTEIQAANGVTDOSPSPQFASVNTTNOA 420
    |||||||
DB 375 cgdnvoyaprqjltleprilyisdlahqlytfeiqangvtdqspisqfasvnltnqa 434
    |||||||
OY 421 APSAIVIMHOVSRVSTILSMQPOPNQVILDYELQYERKLSYKNAFKSPNTVT 480
    |||||||
DB 435 apsaivimhvstrvstltswsqpdqngvildyelqyekerlseynatalkspnlvt 494
    |||||||
OY 481 --GLKKGATYVFOVARTVAGYRGYSGKMFOTMTEAEVOTSIQEKPLITIGSSAGLVE 538
    |||||||
DB 495 vglkagalyvfvartvagyrgyrgkmyfgtmtaeeyqtsiqekpliligsaglyvf 554
    |||||||
OY 539 LIAVVVIAIVCN--RKGPERADSEYTDKLOHTYSGHITPGMKIYIDPPTYEDNEAVEPRA 597
    |||||||
DB 555 liavvialvcnrrrgferadseytdklqhtysghmtpgmkiiydpfityedpneavep 614
    |||||||
OY 598 KEIDISCVKTEQYIGAGEGECVCSGHLKLPGRKEIFVAKITLKSQYTBKORRFLSEASI 657
    |||||||
DB 615 keidiscvkteqyigagegevcsgnhkllpgkreitfvalitlksyvekrtdflseasl 674
    |||||||
OY 658 MGOFDHPNVNTHLEGVVTKSTPVMIIIEFEMENGSLDSFLRONDOGFVYDQVLMRGIAAG 717
    |||||||
DB 675 mgofdhpnvnlhlegvvtksstpvmliitefemengsldeftlqndqgfcvqilvgmlrgiaag 724
    |||||||
OY 718 MKTLADMTYHRLAARNILVNSNLVCKVSDGELSRPLEDTSDPTTSAAGKRPFRWT 777
    |||||||
DB 735 mkyladmnyhrdlaarnilvnsnlvckvsdglsrfldestdpttsaagkrlpfrwt 794
    |||||||
OY 778 APEAIQYRKFTSADWSYGIWMEWVSYGERPYWMDTNDVINAIEQDYLRLPPMDCPS 837
    |||||||
DB 795 apeaiqyrtkftsadwsygiwmevwvsygerpywdmtndvinalieqdyrlppmdcps 854
    |||||||
OY 838 ALHQLMLDCMOKNRNHRKFGQITVTLDKMIRNPNSLKAMAPLSSGINTPLDRTITPDTY 897
    |||||||
DB 855 alhqmldcwqkdrnhpkfegivnltdkmirnpnsikamapssgintplldrtitpdyt 914
    |||||||
OY 898 SEFTVDEMLEAIRMGOYKESFANAGTSPVVSQMMMEDILRGVTLAGQOKILINSIOY 957
    |||||||
DB 915 sftvdeMLEAIRMGOYKESfanaGtspvvsqmmmedilrgvtlagqokilinsiy 974
    |||||||
OY 958 MRAOMNIOSEV 970
    |||||||
DB 975 mraqmqiqsevev 987
    |||||||

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RESULT 4
 AAM26366
 ID AAM26366 standard; Protein; 994 AA.
 AC AAM26366;
 XX
 DT 02-DEC-1997 (first entry)

```

XX DE Mouse Nuk tyrosine kinase.
XX DE Nuk tyrosine kinase; Eph receptor tyrosine kinase;
XX DE signal transduction; axonogenesis; neurodegenerative disease;
XX DE Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX DE multiple sclerosis; amyotrophic lateral sclerosis;
XX DE Wernicke's disease; nerve damage; trauma; ischemia; stroke.
XX OS Mus musculus.
XX FH Key
XX FH Peptide
XX FH Location/Qualifiers
XX FH 1..26
XX FH /label= Sig-peptide
XX FH 27..994
XX FH /label= Mat-protein
XX FH 27..548
XX FH /label= Extracellular_domain
XX FH 330..420
XX FH /label= FNIII
XX FH /note= "fibronectin type III repeat"
XX FH 444..534
XX FH /label= FNIII
XX FH /note= "fibronectin type III repeat"
XX FH 549..574
XX FH /label= Transmembrane_domain
XX FH 575..994
XX FH /label= Cytoplasmic_domain
XX FH 623..888
XX FH /label= Tyrosine-kinase_region
XX PN WO9714966-A1.
XX PD 24-APR-1997.
XX PF 10-OCT-1996; 96WO-CA00679.
XX PR 13-OCT-1995; 95US-0005518.
XX PA (MOON ) MOUNT SINAI HOSPITAL CORP.
XX PI Henkemeyer M, Pawson A;
XX DR WPI; 1997-245245/22.
XX DR N-PSDB; AAT84528.
XX PT Activation of ligand regulatory pathways by Eph subfamily receptor
XX PT tyrosine kinases - for stimulating or inhibiting axonogenesis,
XX PT useful for treatment of e.g. neurodegenerative diseases such as
XX PT Alzheimer's or Parkinson's diseases
XX PS Disclosure: Fig 3; 5;pp; English.
XX CC Murine Nuk tyrosine kinase is an Eph subfamily receptor tyrosine
XX CC kinase that is essential for formation of the medial tract of the
XX CC anterior commissure of the brain, and which appears to play a
XX CC role in the formation of the habenular interneuronal tract. Its
XX CC amino acid sequence was deduced from cDNA clones (see AAT84528)
XX CC isolated from an embryo cDNA library. The extracellular domain
XX CC of Nuk was shown to be sufficient for formation of the medial
XX CC tract. Eph subfamily receptor tyrosine kinases (e.g. the Nuk
XX CC extracellular domain) can be used in claimed methods to: activate
XX CC a ligand regulatory pathway in a cell; identify substances able to
XX CC bind a ligand for an Eph subfamily receptor tyrosine kinase; and
XX CC to affect neuronal development or regeneration, especially the
XX CC stimulation or inhibition of axonogenesis, in a mammal. Activation
XX CC of the ligand regulatory pathway results in downstream activation
XX CC of a series of regulatory pathways in cells that control gene
XX CC expression, cell division, cytoskeletal architecture, cell
XX CC metabolism, cell migration and cell-cell interactions. Substances
XX CC which activate the ligand regulatory pathway may be used for
XX CC stimulating or inhibiting neuronal development, regeneration and
XX CC axonal migration associated with neurodegenerative disease e.g.

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CC Alzheimer's, Parkinson's or Huntington's diseases, multiple
 CC sclerostis, amyotrophic lateral sclerostis, deficiency diseases such
 CC as Wernicke's disease, peripheral nerve damage, trauma and
 CC ischemia resulting from stroke.
 XX

Sequence 994 AA:

Query Match 99.3%; Score 5082; DB 18; Length 994;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

OY 1 LAAAEETLMOSTTAAELGMMVHPSPGMEYSGYDEMNNTIRTYQVCNWESSONMLR 60
 DB 23 Llaaveelmbdctataelgmmvhpssgweevsydenmnlrltygvcnvfessqnnlrl 82
 OY 61 TKFIRRGARHIVHMKFSVRDSSIPSPGCKETFLYYEYEDFSDATPFPMNMP 120
 DB 83 tkfrrrgahrhivemkfsvrdsesipspgcketflnyyeadfdlatkcfpmnmp 142
 OY 121 WKVVTIAADESFQVLDGGRVMTNTEVRSFGVRSGLAFODYGGCSLJAVRVEY 180
 DB 143 wkvtltlaadesfsgvldgrvmkntevrsfgvrsngfyldqdygscsljavrvfy 202
 OY 181 RKPRTIIONGAIFORTLSGAESTSLVARGSCIANAEVNDPIKLCNGDGEMLVPIGR 240
 DB 203 rkprtliongaifortlsgaestslvaarsgclanaevndpiklycngdewlvpiirc 262
 OY 241 MCKAGFEAVENGTCVRCGPGCTFRANOGDEACTHCPIINSRTSGATNCVCRNGYRADL 300
 DB 263 mckagfeavengtcvrcgpgctfrangdeacthcpiinsrtsegauncvcrngyradl 322
 OY 301 DPLMPCTTISARQAVYSSVNETSLMEWTPPPDSGREDLVYNIICKSGSGRGACTR 360
 DB 323 dplmpcttispapqavssvnetslmewtpprdsgrredlvnyllckscsgrgactr 382
 OY 361 CGDNVQYAPROLGLTERRITYSDLAHTOYTFEIOAVNGVTDOSPSPROFASVNTTNOA 420
 DB 383 cgdnvqyaprolglterriytsdlahthoytfeioavngvtdospsprovavnttnoa 442
 OY 421 APSAVSTMHOVSRTVDSITLWSOPDOPNGVILDELOYEKEKLSXNNAVAIKSPNTVT 480
 DB 443 apsavstmhqvstlvdsitlwsopdpngvildeloyekelksxnnavaiksptntvt 502
 OY 481 --GLKAGATVFOYRARTVAGYGRYSGKMYFQMTAEVOTSTIOEKLPLITSSAGLVF 538
 DB 503 vglkagatvfoyrartvagygrysgkmyfqmtaeayotstioeklpllvgsaaglvf 562
 OY 539 LIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHTPGMKIYIDPFYEDPNCAVREPAK 598
 DB 563 llaavvialvcnrrgfesadseytldklohtsghtpgmkityidpfyedpnaavrefak 622
 OY 599 EIDISCKIKIOVIGAGFGFEGVCSGHLKPGKREIIVAIAIKTLKSGYTEKORDELSPASIM 658
 DB 623 eidiscvklievigagfgfegvcsghlpgkreifvaiaiktlksgytekordeleasim 682
 OY 659 GQEDHPNVIHLEGVYKSTPVMITTEPMENGSLDSLRQNDGPFYIOLVGMIRGIAAGM 718
 DB 683 gqedhpnvihlegvykstpvmittetpmsgslslrqndgpfyiolvgmirgiaagm 742
 OY 719 KYLADNMVYVRDLAARNILVNSLVCKVSDFGLSRLEEDTSDPTVTSALGCFPIRMTA 778
 DB 743 kyladnmvyrldlaarnilvnsllvckvsdfgrlreedtsdptvtalslgcfpirmta 802
 OY 779 PEATIORKFTSASDVMSYGVVMEVMSYGEPRYMDTNDVDYINATQDYRLPPMDCPESA 838
 DB 803 peatiorkfthsasdvmsygvvmevmsygerpymdtndvdynatqdyrlppmdcpsa 862
 OY 839 LHOGLMDQCKDRNHRPFGQIVNTLDKMI RNPNSLKAAPLSSGINTLRLRTIPDYTS 898
 DB 863 lhoglmdcqckdrnhprfgqivntldkmlrnpnslkanaplssgintlrlrtipdyts 922
 OY 899 FNVVDMLKAIKMGYKESFANAGFTSFVDVVSOMMEDILRVGVTLACHQKRIINSIQVM 958

DB 923 fntvdmlkaikgkykesfanagfsvdvvsommedilrvgvtlachqkriinsiqvm 982
 OY 959 RAQMNOIOSVEV 970
 DB 983 raqmnoiosvev 994

RESULT 5

ID AAR87018 standard; Protein; 994 AA.

AC AAR87018:

DT 19-MAR-1996 (first entry)

DE Receptor tyrosine kinase (neural kinase).

KM Receptor tyrosine kinase; neural kinase; Nuk; axon;

OS Mus musculus.

Key Location/Qualifiers

FT Peptide 1..26

FT Region 27..548

FT /label= "Extracellular_region
 /note= "The extracellular region (amino acids 27-548) includes an N-terminal Ig-like domain and an Ig-like Nuk repeat"

FT Region 330..420

FT /label= "FNIII

FT Region /note= "fibronectin type III repeat"

FT /label= "FNIII

FT /note= "fibronectin type III repeat"

FT Region 549..574

FT /label= "Transmembrane_region

FT Region 575..994

FT /label= "Cytoplasmic_region

FT Domain 623..707

FT /label= "Tyrosine-kinase_catalytic_domain

PN WO9530326-A1.

PD 09-NOV-1995.

PR 28-APR-1995; 95WO-CA00254.

PR 29-APR-1994; 94US-0235407.

PA (MOUN) MOUNT SINAI HOSPITAL CORP.

PI Henkemeyer M, Letwin K, Pawson A;

DR WPI; 1995-393299/50.

DR N-PSDB; AAT07308.

PT DNA encoding neural receptor tyrosine kinase - useful in gene

PT therapy of nerve disorders, and for diagnosis and identification of

PT therapeutic agents

Claim 1; Page 70-74; 103pp; English.

A novel receptor tyrosine kinase (AAR87018), designated neural kinase (Nuk) (AAR87018), is encoded by cDNA (AAT07308) obtd. from a mouse embryo library. Nuk is expressed in migrating axons and is involved in cell-cell interactions and axonogenesis in development of the nervous system. Nuk or its fragments (pref. amino acids 26-548 or 601-994) are used to identify (ant)agonists of the (activated) receptor tyrosine kinase as a means of treating nerve disorders and damage, or to raise antibodies used to monitor axon

CC migration and nerve cell interactions.

XX Sequence 994 AA:

Query Match 99.3%; Score 5078; DB 16; Length 994;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 963; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

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QY 1 LLAAVEETLMDSTTAAELGMMVHPPSGMEEVSGYDENMNTIRTYOVAVPESSONMLR 60
   |||
DB 23 llaaveelmdstlaaelgmmvhpssgweevsgydenmnlrtlyqvcnfessqnmwlr 82
QY 61 TKFIRRGARHRIHVEKKFSVRDCSSIPSPGSKETFNLYYEADPDSATKTFPMNMENP 120
   |||
DB 83 tkfrrrgarhrihvekkfsvrdcssipspgsketfnlyyyeadpdsatktfpmnmep 142
QY 121 WVKVDTIAADESFQYDLGRVVKITEVRSFGPVSRSGFYLAFODYGGCMLIAVRVY 180
   |||
DB 143 wkvdtlaadesfsqydlgrvvnkitevrsfgpvrsrgfyiafdyggcmliaavrly 202
QY 181 RKCPRRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPVIGRC 240
   |||
DB 203 rkcprriongaifqetlsgaestsivaargscianaevdvpiklycngdgelvpigrc 262
QY 241 MCRAGEFAVNGIVYCRGCGPSTFKANOGDEACTHCPINSRTTSEGATNCVCRNGYRADL 300
   |||
DB 263 mckagfeavngivcrvcgpcgstfkangdeacthpcinsrttsega tncvcrngyyradl 322
QY 301 DPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGRDLVYNTICKSCSGRGACTR 360
   |||
DB 323 dplmpcttlpsaqavissvnetslmlewcprdsgrdelvynlickscsgrgactr 382
QY 361 CGDNVQYAPRQGLGLEPRRIYISDLAHTQYFETIQAVNGVTDGSPSPQFASVNTITNQA 420
   |||
DB 383 cgdnvqyaprqglgleprriyisdlahthqyfetiqavngvtdgspspqfasvntitnqa 442
QY 421 APSAVSTIMHOYKRTVDSITITSMSPDOPNGVIIDYELQYKEKELSEYNATAISPTVTW 480
   |||
DB 443 apsavstihoykrtvdsititmspdopngviidylelykekelseyenataiskptvtw 502
QY 481 -GLKAGAIYFQYARFARVAGYRGYSKMYFQWTAEAYTQSIOEKLPLTIGSSAAGLVF 538
   |||
DB 503 vglkagaiyfqrarfvagyrgryskmyfqwtaeaytqsioeklpllvssaaaglvf 562
QY 539 LIAAVVTAIVCNRGFERADSEYTDKLOHTTSGHITPGMKIYIDPFTYEEDPNEAVREFAK 598
   |||
DB 563 liaavvtaivcnrgferadseytcdkqhlytsghmtpgmkliyidpftyedpneavrefak 622
QY 599 EIDISCVYIEQYVIGAGEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDLFEASIM 658
   |||
DB 623 eidiscvyleqyvigagegvcshlklpgrkelfvaiktlksgytekorrdlfeasim 682
QY 659 GQFHPNVIHLEGVVTKSTPMIITTEFMENGSLDSFLQNDGQFTVITQVLMGLGIAAG 718
   |||
DB 683 gqfhdprnvihlegvvtkstpmiitfefmengsldsflrqndgqftvltqvmglrgiaagm 742
QY 719 KYLADMTVVRHDLAARNTLVNSNLVCKASDGLSRFLEDTPSDPTYSALGCKRPIMWTA 778
   |||
DB 743 kyladmtvvrhdlaarntlvsnlvckvdsdglstrfledtspdptysalgckrplimwta 802
QY 779 PEALIOYRKFTSASDVWSYGIYMMMEVMSYGERPYMDMTNQDIYINAEODYRLPMPDCPSA 838
   |||
DB 803 pealioyrfkftsasdvwsygiymmewmsygerpymdmtntqdinaledgyrlpmpdcpsa 862
QY 839 LHQMLTDCMOKDRNHRPFGQIVNTLDMKIRNPNSLKAMAPLSSGINSPLDRIPIPTYS 898
   |||
DB 863 lhqmltdcmokdrnhrpfgqivntldmkinpnslkamaplsqinspldripipts 922
QY 899 FNTVDEMTLEAIKMGQYKRSFANAGTSPDYVSOMMMEDILVGYTLACHOKILINSIOVM 958
   |||
DB 923 fntvdemtleakmgqykrsfanagtsfdvvsqmmmedilvgytlachokkllnsiovm 982

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QY 959 RAQMNQIOSVEY 970
DB 983 raqmqiosvey 994

RESULT 6

ID AAR75712 standard; Protein: 995 AA.

AC AAR75712;

DT 11-NOV-1995 (first entry)

DE Eph-related PTK Cdk5.

KM Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;

KW prognosis.

OS Gallus sp.

PN W09515375-A.

PD 08-JUN-1995.

PF 07-SEP-1994; 94WO-US10140.

PR 03-DEC-1993; 93US-C162809.

PA (LJOL-) LA JOLLA CANCER RES FOUND.

PI Pasquale EB, Sajjadi FG;

DR WPT: 1995-215256/28.

DR N-PSDB: AAQ90660.

PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing

PS cancer.

PS Disclosure: Page 92-96; 129pp; English.

CC Probes derived from the Eph-related PTKs Cdk4 (AAQ90659) and Cdk5

CC (AAQ90660) were used to isolate novel cDNA clones (AAQ90652-58,

CC AAQ90661-62) from chicken embryo and embryonic brain libraries.

CC Sequence 995 AA:

Query Match 96.8%; Score 4950.5; DB 16; Length 995;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 930; Conservative 28; Mismatches 12; Indels 3; Gaps 2;

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QY 1 LLAAVEETLMDSTTAAELGMMVHPPSGMEEVSGYDENMNTIRTYOVAVPESSONMLR 60
   |||
DB 23 llaaveelmdstlaaelgmmvhpssgweevsgydenmnlrtlyqvcnfessqnmwlr 82
QY 61 TKFIRRGARHRIHVEKKFSVRDCSSIPSPGSKETFNLYYEADPDSATKTFPMNMENP 120
   |||
DB 83 tkfrrrgarhrihvekkfsvrdcssipspgsketfnlyyyeadpdsatktfpmnmep 142
QY 121 WVKVDTIAADESFQYDLGRVVKITEVRSFGPVSRSGFYLAFODYGGCMLIAVRVY 180
   |||
DB 143 wkvdtlaadesfsqydlgrvvnkitevrsfgpvrsrgfyiafdyggcmliaavrly 202
QY 181 RKCPRRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPVIGRC 240
   |||
DB 203 rkcprriongaifqetlsgaestsivaargscianaevdvpiklycngdgelvpigrc 262
QY 241 MCRAGEFAVNGIVYCRGCGPSTFKANOGDEACTHCPINSRTTSEGATNCVCRNGYRADL 300
   |||
DB 263 mckagfeavngivcrvcgpcgstfkangdeacthpcinsrttsega tncvcrngyyrada 322
QY 301 DPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGRDLVYNTICKSCSGRGACTR 360
   |||

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Db 323 dpydmpcttlpsapqavlsenvetslmlewtprdsqaredlynyllckscsggrgactr 382
 QY 361 CGDNVOYAPRQLGTEPRYISDLAHTQYTFEIQAVNGVTDQSPSPFASVNTTNOA 420
 Db 383 cgdhvgfaprtqigltetprlyisdlahltqyltelqavngvtcdqspfpafasvntltng 442
 QY 421 APSAVSIMHOVSTRVSTILSMQDPQNGVILDELYEKELESEYNATAIKSPNTVT 480
 Db 443 apsaavsimhqvstrvstlslsmqdpqngvildelyekeliselstakspntvt 502
 QY 481 --GLKAGATYVFOVRAVTAAGYGRYSKMYFOTMFAEYQTSIOEKPLITISSAAGLVF 538
 Db 503 vgnlkagctlyvfvrtarvaagrysgkmyfgumtaeayqtsvqeklplilgssaaaglvf 562
 QY 539 LIAVVVIAIVCN-RGFERADSEYTDKLOHYTSGHITTPGKTIYIDPFTYEDPNEAVREFA 597
 Db 563 liavvvliivcnrrtgferadseytdklqhytsghmtpgmklyidpftcyedpneavre 622
 QY 598 KEIDISCVKIEBOYIGEGEVCSCGHLKPGKRETFVAIKTKSGYTEKORDFLSEASI 657
 Db 623 keidiscvkiegylgagelgevcsgnlkpgkrelfvaltklksqytekqrdfiseasi 682
 QY 658 MGQFDHPNVIHEGVVTKSTPVMITTEFMENGLSDFLRNDGQFTVITQVGLRGIAAG 717
 Db 683 mgqfdhpnvihnlegvltkespymiltelfmngslsfirndgqftvltqvgmlrgiaag 742
 QY 718 MKYLDMMNVHNDLAARNILVNSNLVCKYSDGFLSRFLEDDTSDPTVTSAIGKFPRIWT 777
 Db 743 mkyldmmnvhndlaarnilvnsnlvckysdfglrflddtsdptvtlsalgygkfpriw 802
 QY 778 APEALQYRKFTSASDVWSYGIWMEVMSYGERPYMDNTNOOVINIKEDDYRLPRMDCPS 837
 Db 803 apealqyrtkftsasdvwsygiwmevmsygerpywmdntnqvlnaleqdyrlprmdcpn 862
 QY 838 ALHQMLDCWQKDRNRHREKFGQIVTLDKMIKRNPSNLKAMAPLSSGINPLIDRTIPDYT 897
 Db 863 alhqmldcwqkdrnrhpkfgqivntldkmltrpnslkamaplsagvnlplldrtclpdyt 922
 QY 898 SFNTDEMLEATKMGQYKESFANGFTSDVYSSOMMEDILRVGVTLAGHOKKILNSIQV 957
 Db 923 sfntdewldeatkmqykesfangaftsdvysommedilrvvgvtlaghokkilstnsiqv 982
 QY 958 MKAQNMQIOSEV 970
 Db 983 mkaqnmqisvev 995

XX WPI: 1995-215256/28.
 DR N-PSDB: AAQ90657.
 XX
 PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
 cancer.
 PS
 CC Claim 11: Page 71-75; 129pp; English.
 CC
 CC A cDNA clone encoding a novel variant of Eph-related protein Cdk5,
 CC Cdk5+ (AAQ90657), was isolated from a chick embryo library in
 CC lambda gt11. Cdk5+ protein (AAR75709) contains a 16-amino acid
 CC insertion in the juxtamembrane domain, and be a result of
 CC alternative splicing. Cdk5+ is exclusively expressed in the CNS.
 CC
 SQ Sequence 1011 AA:

Query Match 96.5%; Score 4934.5; DB 16; Length 1011;
 Best Local Similarity 94.0%; Pred. No. 0;
 Matches 930; Conservative 28; Mismatches 12; Indels 19; Gaps 3;

RESULT 7
 AAR75709 standard; Protein: 1011 AA.
 XX
 AC AAR75709;
 XX
 DT 11-NOV-1995 (first entry)
 XX
 DE Eph-related PTK Cdk5+.
 XX
 KW Cdk5+; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
 KM prognosis.
 XX
 OS Gallus sp.
 PN MO9515375-A.
 XX
 PD 08-JUN-1995.
 XX
 PF 07-SEP-1994; 94MO-US10140.
 XX
 PR 03-DEC-1993; 93US-0162809.
 XX
 PA (JOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Pasquale EB, Sajjad FG;

QY 1 LIAVEETLMDSTATATLGLGMVHPSPGWEVSGYDENMTTIRTYOVCNVESSONMLR 60
 Db 23 liaveetlmdstataetlglgmvhpsgwevsgydenmtlitycvcnfessqnmlr 82
 QY 61 TKFTRRGARHRIHEMKFSVRDCSTPSVPSCKEPFLTYTADPDSATKTPNNMKNP 120
 Db 83 tkftrrgarhrihemkfsvrdcslpnpvpscketfhtlyysddtsaektlpnnmkn 142
 QY 121 WVKVDTIADESFQVDLGRVNMKINTEVRSFGVSRKSGFYLAFOBYGCMSTIAVRVF 180
 Db 143 wkvdtiaadesfsvdldgrvnmkintevrsfgvskngfylafdygycmsliavrvf 202
 QY 181 RKCRITLONCAIHOETLSGAEVSTIYAARSGCTIANEEDVVPKLYCNGDEWLPVIGRC 240
 Db 203 rkcrvltqngavrtelsgaesctsiyaarvgtcismaneedvpiklycngdewlvpg 262
 QY 241 MCRAGEFVAVNGTVCRCPCSGTEKANGDEACTHCPINSTRTEGATNVCWRGVYRADL 300
 Db 263 mcrpyvasvngtvcrcpcsgtkaasgdegcvhcpinsttsegatncvcrngyrad 322
 QY 301 DPLDMCTTTPSAPOAVISSVNETSLMLEWTPRDSGREDLVYNTICKSCSGRGACTR 360
 Db 323 dpydmpcttlpsapqavlsenvetslmlewtprdsqaredlynyllckscsggrgactr 382
 QY 361 CGDNVOYAPRQLGTEPRYISDLAHTQYTFEIQAVNGVTDQSPSPFASVNTTNOA 420
 Db 383 cgdhvgfaprtqigltetprlyisdlahltqyltelqavngvtcdqspfpafasvntltng 442
 QY 421 APSAVSIMHOVSTRVSTILSMQDPQNGVILDELYEKELESEYNATAIKSPNTVT 480
 Db 443 apsaavsimhqvstrvstlslsmqdpqngvildelyekeliselstakspntvt 502
 QY 481 --GLKAGATYVFOVRAVTAAGYGRYSKMYFOTMFAEYQTSIOEKPLITISSAAGLVF 538
 Db 503 vgnlkagctlyvfvrtarvaagrysgkmyfgumtaeayqtsvqeklplilgssaaaglvf 562
 QY 539 LIAVVVIAIVCN-RGFERADSEYTDKLOHYTSGHITTPGKTIYIDPFTYEDPNEAVREFA 597
 Db 563 liavvvliivcnrrtgferadseytdklqhytsghmtpgmklyidpftcyedpneavre 622
 QY 582 DPEFTYEDPNEAVREFAKELDISCVKIEBOYIGEGEVCSCGHLKPGKRETFVAIKTKS 641
 Db 623 dpeftypedneavrefakeidiscvkiegylgagelgevcsgnlkpgkrelfvaltklks 682
 QY 642 GYTEKORDFLSEASIMGQFDHPNVIHEGVVTKSTPVMITTEFMENGLSDFLRNDGQFTVITQVGLRGIAAG 701
 Db 683 gytেকordfliseasimgqfdhpnvihnlegvltkespymiltelfmngslsfirndgq 742
 QY 702 FTVITQVGLRGIAAGMYKYLADMMNVHNDLAARNILVNSNLVCKYSDGFLSRFLEDDTSD 761
 Db 743 ftvitqvgmlrgiaagmkyladmmnvhndlaarnilvnsnlvckysdfglrflddtsd 802

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OY 762 PRTYSALGKFKPIRMTAPEAIOVRKFTSADVSYIVAMEVMSYGERPYMDTNDQVIN 821
DB 803 PRTYSALGKFKPIRMTAPEAIOVRKFTSADVSYIVAMEVMSYGERPYMDTNDQVIN 862
OY 822 AIBODRLRPPMDCPALHOLMLDCWOKDRNHRKFGQIVNTLKKIIRNPNSIKAMAPIS 881
DB 863 AIEGDYRLPPMDCPALHOLMLDCWOKDRNHRKFGQIVNTLKKIIRNPNSIKAMAPIS 922
OY 882 SGINULPLDTRIDYTSFNIVDEMLAIKMGYKESFANAGFTSPYVSQMMEDILRAG 941
DB 923 SGYNLPLDTRIDYTSFNIVDEMLAIKMGYKESFANAGFTSPYVSQMMEDILRAG 982
OY 942 VTLAGHOKILNSIQVRAQMOQIOSEYV 970
DB 983 VTLAGHOKILNSIQVRAQMOQIOSEYV 1011

RESULT 8
AAR44513
ID AAR44513 standard; Protein; 984 AA.
AAR44513:
XX AC AAR44513:
XX DT 16-JUN-1994 (first entry)
XX DE elk.
XX KW Lambda gtl1: expression vector; lambda-BI-Elk: protein tyrosine kinase;
XX KM Elk; BI: Eph; subfamily; receptor-like tyrosine kinase; eph: eck;
XX KW phosphorylation; phosphorylated kinase insert domain; growth factor;
XX KM receptor kinase; platelet-derived growth factor receptor.
XX OS Rattus rattus.
XX PH Key Location/Qualifiers
XX FT Peptide 1..17 "Signal peptide"
XX FT MISC-difference 61 /note= "Cysteine residue"
XX FT MISC-difference 96 /note= "Cysteine residue"
XX FT MISC-difference 106 /note= "Cysteine residue"
XX FT MISC-difference 183 /note= "Cysteine residue"
XX FT MISC-difference 196 /note= "Cysteine residue"
XX FT MISC-difference 225 /note= "Cysteine residue"
XX FT MISC-difference 240 /note= "Cysteine residue"
XX FT MISC-difference 253 /note= "Cysteine residue"
XX FT MISC-difference 255 /note= "Cysteine residue"
XX FT MISC-difference 267 /note= "Cysteine residue"
XX FT MISC-difference 270 /note= "Cysteine residue"
XX FT MISC-difference 284 /note= "Cysteine residue"
XX FT MISC-difference 287 /note= "Cysteine residue"
XX FT MISC-difference 301 /note= "Cysteine residue"
XX FT MISC-difference 303 /note= "Cysteine residue"
XX FT MISC-difference 319 /note= "Cysteine residue"
XX FT MISC-difference 360 /note= "Cysteine residue"
XX FT MISC-difference 363 /note= "Cysteine residue"

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FT FT /note= "Cysteine residue"
FT MISC-difference 370 /note= "Cysteine residue"
FT MISC-difference 373 /note= "Cysteine residue"
FT Modified-site 425..427 /note= "N-glycosylation site"
FT Modified-site 480..482 /note= "N-glycosylation site"
FT FT CA2083521-A.
PD 01-OCT-1993.
PF 23-NOV-1992; 92CA-2083521.
PR 31-MAR-1992; 92US-0861390.
XX (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX Letwin K, Panson A, Reedijk M;
XX WPI; 1993-406300/51.
XX DR N-PSDB; Q753471.
XX Expression of phosphorylated exogenous protein - in host cells
XX transformed with two vectors, one for the protein, the other for
XX catalytic domain of protein kinase
XX PS Disclosure; Fig 3; 53pp; English.
XX CC This sequence is encoded by the elk cDNA and represents the protein
XX tyrosine kinase, elk. The Elk gene, BI, encode a protein which is
XX a member of the eph subfamily of protein tyrosine kinases. The Elk
XX product is very similar to two other receptor-like tyrosine kinases,
XX eph and eck. Lambda-BI-Elk may be used in the production of
XX phosphorylated exogenous protein along with a further vector encoding
XX the desired exogenous protein. These plasmids may be used to produce
XX phosphorylated proteins in host cells which have no intrinsic capacity
XX for phosphorylation, eg. bacteria. The system may be used for the
XX expression of the phosphorylated kinase insert domain of a growth
XX factor receptor kinase eg. platelet-derived growth factor receptor.
XX SQ Sequence 984 AA:

Query Match 76.4%; Score 3906.5; DB 14; Length 984;
Best Local Similarity 73.9%; Pred. No. 3.3e-285;
Matches 716; Conservative 128; Mismatches 122; Indels 3; Gaps 2:

OY 2 LAAVEETIMDSTATAELGMVHPPSGWEVSGYDENMNTIRTYOVYCNVPESQNNMLRT 61
DB ::::|||||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||: 74
OY 62 KPIRRGAKRIHYEMKFSVNDCCSISVPSCKETNIVYEADPFDSAVKTPPNWENPM 121
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 134
OY 75 ffltrgahriylemrtfvdcsilpnyvpsckethllyyvedsvlatkksafseapy 134
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 194
OY 122 VKVDTIADSEFSQVDDGCHVMKINTEVRSFGVSRSGEYLAFODYGCMSLIAVREYR 181
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 194
OY 182 KCPRIIONGAIFDETLSGASTSLVAARGSCIANAEVYVPIKLYCNGGCEMLVPIGRCM 241
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 254
OY 195 kcpelvgnfavfepelmgaestsivlarietcpinaeevdpiklycngdgemvpiqrct 254
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 301
OY 242 CKAFEEAVENGTVQFGSGFTFKANOGDEACTHOPINSRTSGATNCVCRNGYRADLD 301
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 313
OY 255 ckagyp-ensvackacpqrtrkasgeagcsncpsnrsrpsaplcortlyradfd 313
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 361
OY 302 PLDMPCYTIIPSAQAVTSSVNETSLMLEWTPPRDSGGREDLVYNIICKSGSGRGACTRC 361
DB ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 373
OY 314 pvevactsvpgrnrvvisivnetstillewppretelgrdvtnylickkcradrtscsc 373
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 362 GDNVQAPROGLTEPRITISDLAHTQYTFEIQAVNGVTDSPSPQFASVNTTQNA 421
DB 374 ddvvefvrpqglglecrvslswahtpyctfdlqalngvsakspmpqhvsnltcngaa 433
QY 422 PSAVSIHNOVSRTVDSITLSMSQPOPNVILDELYQYKEKLSXNATAISPTNT--V 479
DB 434 psrvplmbhvsatmslilswpqpqngllldyeltlyekhefnsmarsqntarl 493
QY 480 TGLKAGAVFQVARTVAGRYSGKMYFQTMTEAETYSIOEKLPILIGSSAGLVFL 539
DB 494 dgflprgmvyvrvartvaygkfsgkmsfgcltdddykselrqlpllagsaaqvvfv 553
QY 540 IAVVYVIAICNRRGFERADSEYTDKLOHTSGHITPGMKIYIDPPTYEDPNEAREFAKE 599
DB 554 vslvalsvcarckrayksaavysdklqhytstgrspgmkiyldpfctydpneavrefake 613
QY 600 IDISCVKIEQVIGAGEFGEVCSGHLKPGKREIFAIVTKISGYTEKORROPLSFASIMG 659
DB 614 ldvstfvlkleevlgaggefgevykgriklpqkrelyvalklkagyskqgrdfllsaasimg 673
QY 660 QPDHPNVHLBEGVTKSPVWITTEFMENGSLDSFLRONDQFTVILVGMRLGIAAGMK 719
DB 674 qdhpnlrlrlegvvtcksrpvmlltefmgngaldsflrqnqdgftvqlvgmlrglaagmk 733
QY 720 YIADNNVYHRLAARNILVNSNLVCKVSDFGSLRLEDDTSDPTYSALGSKFPRIWTA 779
DB 734 ylsennmyhrdlaarlnllvnsnlvckvsdfglstrylqddtsdpclytslsgkklpvrwtap 793
QY 760 EAIQVRFKTSADVWSYGIIVMVEVMSYGERPYMDNDVINAIEODYRLRPPMDCPAL 839
DB 794 ealvrfktsasdvwsyglvmewmsfgerpyvdmnsqdvlnaleqdyrlppmdcpaal 853
QY 840 HOLMDCQKORNRHPRKGGQIVNTLDKMI RNPNLSLKAMAPLSSGINDPLDRTIPDYTSF 899
DB 854 hqlmldcwqkdrnprfaelivntldkmlrnpaslkltvalrtaypsqplldrsipdtatf 913
QY 900 NTVDEMLFAIMGOYKESEFANAGFTSPDVYSOMMEIOLKRGVTLAAGHOKKILNSIOVM 959
DB 914 ctvdvwlaklmvgvyrdfllagfctslqvlvcqmtsedllrtlyvclagbhqkklisslmsr 973
QY 960 AQMNQIOGV 968
DB 974 vqmqnspav 982

RESULT 9
AAR75704
ID AAR75704 standard; Protein: 951 AA.
XX
AAR75704:
XX
DT 11-NOV-1995 (first entry)
XX
DE Eph-related CEK6.
XX
KM Cek6; Eph: protein tyrosine-kinase; PTK; cancer; diagnosis:
XX
XX prognosis.
XX
OS Gallus sp.
XX
FH Key Location/Qualifiers
FT Domain 426..444
XX /Label= Extracellular_domain
PN MO9515375-A.
XX
XX
PD 08-JUN-1995.
XX
XX 07-SEP-1994; 94WC-US10140.
XX
XX 03-DEC-1993; 93US-0162809.
XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Pasquale EB, Sejtadi FG;
XX
DR WPL: 1995-215256/28.
XX
DR N-PSDB: AAC90652.
XX
PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
PT cancer.
XX
PS Claim 12; Page 37-41; 129pp; English.
XX
XX
CC Novel Eph-related PTK Cek6 cDNA clones (AA090652) were isolated from
CC chick embryo and embryonic brain cDNA libraries in phage lambda gt11.
CC The encoded Cek6 protein (AAR75704) is closely related to rat Elk,
CC Cek5 (AAR75712) and Cek10 (AAR75708). Cek6 transcripts were found in
CC 10-day embryos and in adult brain, lung, heart and skeletal muscle.
XX
SQ Sequence 951 AA;
QY 7 ETLMDSTTATAEIGMMVHPSPGMEEVSGDENMTIRTYOVGVPPSSQNNMLRTKFIIR 66
Best Local Similarity 70.1%; Score 3698.5; DB 16; Length 951;
Matches 686; Conservative 120; Mismatches 118; Indels 55; Gaps 4;
DB 1 etlmdsttataeigvrcanpssvwevsygydenlrltyqvcnvtapnqnnvlltflnr 60
QY 67 RGAHRLHVENKFSRDCSSIPSVGSKETFNLYYEADFDSATKTFPMNMENPVKVD 126
DB 61 rghrlrlytemrfvrddsslpnvgscketfnlyyywidsvlatkksatfcapylkvt 120
QY 127 IADDESQVDGGRVWKINTFVRSFVRSRGFTYLAFDYGGCSLAVRVFYRKCPRI 186
DB 121 iaadesfsqvdggrlwk-----gfxfkcpv 147
QY 187 IONGALFOETLSGAEISTVLAARSCIANAEYDPIKLYCNGDGEWIVPIRCCKXGF 246
DB 148 vqfalfpemlmgaeestslvtargtlcplnaeevdpklkycngdgemvplvrcckxgy 207
QY 247 EAVENGTVCRCPSGTFKANKQDEACTHCPINSRTTSEGATNCVCRNGYVRADLPDMP 306
DB 208 ep-ennvactrcpactgfkasgagjlcrcpnrssaaesplcacnryfiredlprpca 266
QY 307 CTTPSPQAVISVVENSTLMLBMPPRDSGGRREDLVNITCKSGSGRGACTRCGDNVQ 366
DB 267 ctsvpsgprnvslsvneusillempreclgrddvlynlvckkcradrtccsrdhve 326
QY 367 YAPROLGLTEPRITISDLAHTQYTFEIQAVNGVTDSPSPQFASVNTTQNAAPSAVS 426
DB 327 fvrpqgltefvrlswahtpyctfdlqalngvsakspmpqhvsnltcngaa 386
QY 427 IMHOVSRTVDSITLSMSQPOPNVILDELYQYKEKLSXNATAISPTNT--V 479
DB 387 lmbhvsatmslilswpqpqngllldyeltlyekhefnsmarsqntarl 446
QY 468 NATAIKSPNT--VTGLAGAVFQVARTVAGRYSGKMYFQTMTEAETYSIOEKLPILIG 525
DB 447 nsvvargnterleqlrpgmvyvrvartvaygkfsgkmsfgcltdddykselrql 506
QY 526 PLITSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHITPGMKIYIDP 585
DB 507 pllagsaaqvvfvlsvlsvcarckrayksaavysdklqhytstgrspgmkiyldpf 566
QY 586 YEDPNEAREFAKEITDISCVKIEQVIGAGEFGEVCSGHLKPGKREIFAIVTKISGYTE 645
DB 567 yedpneavrefakeitdvsvlkleevlgaggefgevykgriklpqkrelyvalklkagys 626
QY 646 KQRDPLSEASIMGFDHPNVIHLEGVTKSTPMIITTEFMENGSLDSFLRONDQFTV 705
DB 627 kqrdfllsaasimgfdhpnlrlrlegvvtcksrpvmlltefmgngaldsflrqnqdgftv 686

DT 11-NOV-1995 (first entry)
 XX Eph-related PTK Cck10+.
 DE Cck10+: Eph: protein tyrosine-kinase; PTK; cancer; diagnosis;
 KM prognosis.
 XX Gallus sp.
 OS WO9515375-A.
 PN 08-JUN-1995.
 PD 07-SEP-1994: 94WO-US10140.
 PE 03-DEC-1993: 93US-0162809.
 PR (LJOL-) LA JOLLA CANCER RES FOUND.
 PA Pasquale EB, Sajjadi FG.
 PI WPI: 1995-215256/28.
 DR N-PSDB: AA090658.
 DR Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
 PI cancer.
 PT Claim 11; Page 78-82; 129pp; English.
 PS Novel Eph-related PTK cDNA clone Cck10 (given in AA090656) and a
 CC variant clone, Cck10+ (AA090658), whose product contains a 15-amino
 CC acid insertion in the juxtamembrane domain, were isolated from a
 CC chick embryo library in lambda gt11. Cck10 and Cck10+ may
 CC originate from the same gene by alternative splicing. Cck10
 CC expression was prominent in the kidney, and to a lesser extent in
 CC the lung.
 XX
 XX Sequence 988 AA:

Query Match 71.38; Score 3649.5; DB 16; Length 988;
 Best Local Similarity 70.0%; Pred. No. 7.2e-266;
 Matches 683; Conservaltive 120; Mismatches 144; Indels 29; Gaps 6;

QY 16 TAEIAGMAYPPSGMEVGYDENMNTITRYOVAVFESSQNNMLRTFIRRGARHIVE 75
 DB 21 tselawtchpceygeewsygydeamplrtcygvcnvreaqnwlrtkfflqrdvqryve 80
 QY 76 MKEFVRDCSSIPSVPGSKETFNLYYEADFDSATKTTPNMENPMWVKVPTIADSESQ 135
 DB 81 kftvrdcnsipnlpgcketfnlfyesdtsasanspfmtenpylkvdtladpdesfsk 140
 QY 136 VDLGGRVAKITVEVRSRSPVRSRSGFYLAFODYGGCNSLIARVRFKRCPRIONGATFOE 195
 DB 141 lesg---rvntkvrstfpglskngfyafqdl9acmclisvratfkykcsntlaegfalffe 196
 QY 196 TLSCAESTSLVAAGSCIANAEEDVPIKLYCNGDGMVPIGCMCKAKFEAVENTVC 255
 DB 197 tlgaepslvlapgtcnpavevsvplklycngdgemvpygactcaagyepamkdtgc 256
 QY 256 RGCSSGTFKANGDEACTHCPINSRTTSEGATNCVCRNGYRADLPDLMPCTTIPSAPO 315
 DB 257 qacpgpfkfskqegpcpcpnarcttagaatvcicrsffiradadpadsacsypsapr 316
 QY 316 AVISSVNETSLMLEMTPPRDSGREDLVYNIICKSCSGSGACTRCGDNVQVAPROL--- 372
 DB 317 svlnvvetatvlewsepqdagrdldlylvnlickcseverrlscrcddnvefvrqgl 376
 QY 373 GLTEPRIVIDLAAHTQYFEIQAVNGVTQSPSPQFASVNTTNOAPSAVSIMHVS 432
 DB 377 glteritlylckvmahpvyfteiqavngisakpphfaevnltnqaepsvapcmhlns 436
 QY 433 RTVDSTILMSQPDQNGVILDLVELOYEKE-LSEYNATRAIKSPNTV--TGKKAQATV 489

DB 437 stgnmtlswcpberpnglildyelkysekqggdglantvctsknsvrldglikanarym 496
 QY 490 FOVARRTAVAGRYSGKAYFQMTAEAYQTSIOEKPLTISSAAGVFLAVAVIAYVC 549
 DB 497 qvratavagyryslpreftlaedgstsktfqelplygsatcagllfvlvvlavlc 556
 QY 550 NRRCF-----ERADSETDKLQHTYSGHITPCKMITYIDPFTYEDPNEAVR 594
 DB 557 ftkgmvtceqlssplgrtkgrnstldpeyteklygy-----vprgmkyldpfyedpneavr 612
 QY 595 EFAEKIDISCVKIEOVIGAGEFEGVCSGHLKLPCKREIFAIAIKTKSGYREKORPDLSE 654
 DB 613 efakeidiscvkieevigagefegvcrglklpgrtelvvalklkvylvergrdtlse 672
 QY 655 ASIMGQDPHNVHLEGVYTKSPVMTITERMENGSLDSFLRONDQGFVYIQLVGMRLGT 714
 DB 673 asimgqfthpnlhlegvvtksrprwlltefemencalidsflrlndgqfvcqlvgmrlgt 732
 QY 715 AAGMKYLADMYVHRDLAARNILVNSNLCKVSDFGLSRLEDDTSDPYTTSLGSKFPI 774
 DB 733 aagmkylsemmyvnrtdlaarnllvnsnlckvsdfglsrleddpdpdpcytsal9gkkipi 792
 QY 775 RWTAPRALQYRKFTSASDVNSYGIWMWENASYGEPYMDWTNODVINAIRPDRPLPMD 834
 DB 793 rwtapealrkykftsasdvwsyglwmwensygerpywmsngdvlnaveqdyrlppmd 852
 QY 835 CPBALHOLMLDCKQKRNHRPRFGQIVNTLDKMRPNPSLKAPAPLSSGINTPLDRTIP 894
 DB 853 cpbalhmlldcwvrrdtnlprkfaglvntldkllrtnaaslkvasvgvsqplldrtyp 912
 QY 895 DYSFNTVDEMLAIIKIKQYKESFANAGFTSPVVSOMMEEDILRGVYLAGHOKKILNS 954
 DB 913 dytftvtvgwldakimgrykenfnvagfaslvdvaqmcaedllrlgvtlaqhqkllss 972
 QY 955 IQVRAQMNQIOSVEV 970
 DB 973 lqdmrlqmqnqlpvy 988

RESULT 12
 ID AAR51899 standard; Protein; 990 AA.
 XX AAR51899;
 AC AAR51899;
 XX 09-NOV-1994 (first entry)
 DT Human embryonal kinase 2 receptor.
 DE Embryonal kinase; HEK; protein tyrosine kinase; PTK; tumour;
 KM cancer; therapy; amplification; primer; polymerase chain reaction;
 KW PCR.
 OS Homo sapiens.
 XX DE4233782-A.
 PN 14-APR-1994.
 PD 07-OCT-1992: 92DE-4233782.
 PE 07-OCT-1992: 92DE-4233782.
 PR 07-OCT-1992: 92DE-4233782.
 XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.
 PA Holtrich U, Ruebsamen-Waligmann H, Streibhardt K;
 PI WPI: 1994-127194/16.
 DR N-PSDB: AA062461.
 DR Human embryonal kinase 2-receptor protein - useful in tumour
 PT diagnosis and therapy

Sequence 990 AA;

9

Db 979 r1qmqtlpvqv 990

Wed Jul 25 13:03:56 2001

us-09-378-759-11.rag

Page 15

Db 959 qlmkvhlnglpev 973

Search completed: July 24, 2001, 16:28:46
Job time: 417 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:29:14 ; Search time 14.81 Seconds

(without alignments)
2243.607 Million cell updates/sec

Title: US-09-378-759-11

Sequence: 1 LIAVEETLMDSTTATLGLG.....ILNSIQVRAQNMQIOSVEV 970

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5089	99.5	1055	1	EPB2_HUMAN
2	5082	99.3	993	1	EPB2_MOUSE
3	4932.5	96.4	1004	1	EPB2_CHICK
4	4902	95.8	987	1	EPB2_COTJA
5	3914.5	76.5	984	1	EPB1_RAT
6	3899.5	76.2	984	1	EPB1_HUMAN
7	3754	73.4	985	1	EPB1_XENLA
8	3704	72.4	984	1	EPB1_CHICK
9	3649.5	71.3	988	1	EPB3_CHICK
10	3632.5	71.0	998	1	EPB3_HUMAN
11	3604	70.4	993	1	EPB3_MOUSE
12	3593.5	70.2	902	1	EPB3_XENLA
13	3465.5	65.3	1002	1	EPB3_CHICK
14	3341.5	60.0	986	1	EPB4_XENLA
15	3070	59.8	985	1	EPB4_XENLA
16	3060.5	59.5	986	1	EPB4_CHICK
17	3042	59.2	993	1	EPB4_HUMAN
18	3031	59.2	993	1	EPB4_MOUSE
19	3026.5	59.2	993	1	EPB4_CHICK
20	3026	59.0	998	1	EPB4_MOUSE
21	3016	58.9	998	1	EPB4_HUMAN
22	3014	58.7	998	1	EPB4_MOUSE
23	3001	58.7	998	1	EPB4_MOUSE
24	3001	58.7	998	1	EPB4_MOUSE
25	2990	58.4	1013	1	EPB3_CHICK
26	2918.5	57.0	983	1	EPB3_HUMAN
27	2914	56.8	983	1	EPB3_CHICK
28	2904	56.7	984	1	EPB3_RAT
29	2902	56.7	984	1	EPB3_RAT
30	2875.5	56.2	983	1	EPB3_MOUSE
31	2840.5	55.5	981	1	EPB3_BRARE
32	2835.5	55.4	987	1	EPB4_MOUSE
33	2811	54.9	1035	1	EPB6_MOUSE

ALIGNMENTS

RESULT	ID	EPB2_HUMAN	STANDARD:	PRT:	1055 AA.
AC	P29323	043477			
DT	01-DEC-1992	(Rel. 24, Created)			
DT	01-OCT-2000	(Rel. 40, Last sequence update)			
DT	01-OCT-2000	(Rel. 40, Last annotation update)			
DE	EPHRIIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EPH-3) (DRT) (RECEPTOR PROTEIN-TYROSINE KINASE HEK5) (ERK).				
DE	EPHB2 OR EPHB3 OR ERK OR DRT OR HEK5.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=96154673; PubMed=8589679;				
RA	Ikegaki N., Tang X.X., Liu X.-G., Biegel J.A., Allen C., Yoshioaka A., Sulman E.P., Brodeur G.M., Pleasure D.E.;				
RT	"Molecular characterization and chromosomal localization of DRT (EPH3): a developmentally regulated human protein-tyrosine kinase gene of the EPH family.";				
RL	Hum. Mol. Genet. 4:2033-2045(1995);				
RN	[2]				
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).				
RC	TISSUE=Gastric carcinoma;				
RX	MEDLINE=93343925; PubMed=7688222;				
RA	Iwase T., Tanaka M., Suzuki M., Naito Y., Sugimura H., Kino I.;				
RT	"Identification of protein-tyrosine kinase genes preferentially expressed in embryyo stomach and gastric cancer.";				
RL	Biochem. Biophys. Res. Commun. 194:698-705(1993).				
RN	[3]				
RP	SEQUENCE FROM N.A. (LONG ISOFORM).				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=98359217; PubMed=9696046;				
RA	Tang X.X., Pleasure D.E., Brodeur G.M., Ikegaki N.;				
RT	"A variant transcript encoding an isoform of the human protein tyrosine kinase EPHB2 is generated by alternative splicing and alternative use of polyadenylation signals.";				
RL	Oncogene 17:521-526(1998).				
RN	[4]				
RP	SEQUENCE OF 15-986 FROM N.A. (SHORT ISOFORM).				
RC	TISSUE=Brain;				
RX	MEDLINE=95206782; PubMed=7898931;				
RA	Fox G.M., Holst P.L., Chute H.T., Landberg R.A., Janssen A.M.,				
RT	"cDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine kinases.";				
RL	Oncogene 10:897-903(1995).				
RN	[5]				
RP	SEQUENCE OF 509-986 FROM N.A. (SHORT ISOFORM).				
RC	TISSUE=Brain;				
RA	Saito T., Neohiko S., Kishihara M., Murata M., Yamamoto Y.,				
RL	Hori T., Matsuda Y.;				

34	2799.5	54.7	987	1	EPB4_HUMAN	P54760 homo sapien
35	2650	51.8	1004	1	EPB6_MOUSE	O09127 mus musculu
36	2600	47.8	948	1	EPB6_RAT	P54758 rattus norv
37	2446	40.8	1014	1	EPB6_MOUSE	O08644 mus musculu
38	2442	47.7	877	1	EPB5_MOUSE	O06629 mus musculu
39	2438	47.7	1006	1	EPB6_HUMAN	O15197 homo sapien
40	2349.5	45.9	976	1	EPB2_HUMAN	P29317 homo sapien
41	2340.5	45.7	976	1	EPB2_MOUSE	O03145 mus musculu
42	1905.5	37.2	976	1	EPB1_HUMAN	P21709 homo sapien
43	1648	32.2	500	1	EPB3_BRARE	O13147 brachydantio
44	1197.5	23.4	372	1	EPB8_RAT	P29321 rattus norv
45	1187.5	23.2	292	1	EPB4_BRARE	O13148 brachydantio

RL Submitted (Aug-1994) to the EMBL/Genbank/DBJ databases.
 RP [6] SEQUENCE OF 652-712 FROM N.A.
 RX MEDLINE-91296384; PubMed-1648701;
 RA Chan J., Walt V.M.;
 RT "eek and erk, new members of the eph subclass of receptor protein-
 tyrosine kinases";
 RL Oncogene 6:1057-1061(1991).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 910-966 (SHORT ISOFORM).
 RX MEDLINE-99132419; PubMed-9933164;
 RA Thawes C.D., Goodwill K.E., Bowie J.U.;
 RT "Oligomeric structure of the human EphB2 receptor SAM domain.";
 RL Science 283:833-836(1999).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. THE LIGAND-
 ACTIVATED FORM INTERACTS WITH MULTIPLE PROTEINS, INCLUDING GTPASE-
 ACTIVATING PROTEIN (RASGAP) THROUGH ITS SH2 DOMAIN. RASGAP BINDS
 EPHB2 THROUGH THE JUXTAMEMBRANE TYROSINES RESIDUES (BY
 SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
 PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM/EPHB2V (SHOWN HERE)
 AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: BRAIN, HEART, LUNG, KIDNEY, PLACENTA,
 PANCREAS, LIVER AND SKELETAL MUSCLE. PREFERENTIALLY EXPRESSED IN
 FETAL BRAIN.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 RECEPTOR SUBFAMILY.
 CC -----
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 entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: LA1939; AAA99310.1; -;
 DR EMBL: D31661; BAA06506.1; -;
 DR EMBL: AF025304; AAB94602.1; -;
 DR EMBL: D14717; BAA03537.1; -;
 DR EMBL: L36643; AAA74244.1; -;
 DR EMBL: D37827; BAA07073.1; -;
 DR EMBL: X59292; CAA41981.1; -;
 DR PDB: 1BAF; 16-FEB-99.
 DR MIM: 600997; -;
 DR InterPro: IPR000561; -;
 DR InterPro: IPR000719; -;
 DR InterPro: IPR001090; -;
 DR InterPro: IPR001245; -;
 DR InterPro: IPR001426; -;
 DR InterPro: IPR001660; -;
 DR InterPro: IPR001777; -;
 DR Pfam: PF01404; BPH_1bd; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00014; FNTYPEP11.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRINTS: PR00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00109; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN; 1.
 DR Transferrin: Tyrosine-protein kinase: ATP-binding; Phosphorylation;
 Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure;
 KW Alternative splicing; Repeat.
 FT SIGNAL 1 18
 FT CHAIN 19 1055 EPHRIN TYPE-B RECEPTOR 2.

FT	DOMAIN	19	543	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	544	564	POTENTIAL.
FT	DOMAIN	565	1055	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	184	324	CYS-RICH.
FT	DOMAIN	436	418	FIBRONECTIN TYPE-III.
FT	DOMAIN	436	520	FIBRONECTIN TYPE-III.
FT	DOMAIN	621	884	PROTEIN KINASE.
FT	DOMAIN	911	986	SAM.
FT	SITE	984	986	PDZ-BINDING MOTIF (POTENTIAL) (IN SHORT
FT	NP_BIND	627	635	ISOFORM).
FT	BINDING	653	653	ATP (BY SIMILARITY).
FT	ACT_SITE	746	746	ATP (BY SIMILARITY).
FT	MOD_RES	596	596	BY SIMILARITY.
FT	MOD_RES	602	602	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD_RES	780	780	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD_RES	930	930	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	CARBOHYD	265	265	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	336	336	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	428	428	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	482	482	G -> V (IN SHORT ISOFORM).
FT	VANSPPLIC	986	986	MISSING (IN SHORT ISOFORM).
FT	VANSPPLIC	987	1055	A -> R.
FT	VARIANT	671	671	/FTID-VAR_004162.
FT	CONFLICT	1	20	MALRIGALALLPLLAIVE -> MMYVIALPVCYIA
FT	CONFLICT	154	154	(IN REF. 2).
FT	CONFLICT	476	476	G -> D (IN REF. 2).
FT	CONFLICT	532	532	K -> KO (IN REF. 2).
FT	CONFLICT	495	495	E -> D (IN REF. 2).
FT	CONFLICT	568	568	MISSING (IN REF. 4).
FT	CONFLICT	589	589	R -> RR (IN REF. 1).
FT	CONFLICT	788	788	M -> I (IN REF. 4).
FT	CONFLICT	853	853	I -> F (IN REF. 4).
FT	CONFLICT	923	923	S -> A (IN REF. 2 AND 5).
FT	CONFLICT	936	936	E -> K (IN REF. 2 AND 5).
FT	CONFLICT	958	958	L -> V (IN REF. 3).
FT	CONFLICT	958	958	V -> L (IN REF. 1).
SO	SEQUENCE	1055 AA;	117506 MW;	D0AA2CC8B6CDB8 CRC64;

Query Match 99.5%; Score 5089; DB 1; Length 1055;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 966; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
 1 LLAAYEETLMDSTTATAELGMMVHPSPGWEVSGYDENNTIRTYOVGVNVESSQNNMLR 60
 15 LLAAYEETLMDSTTATAELGMMVHPSPGWEVSGYDENNTIRTYOVGVNVESSQNNMLR 74
 61 TKFIRRRGAHRIHVEKFFSVROCSSIPSPVSGCKETFNLYYEADPDSATKTFPMMEHP 120
 75 TKFIRRRGAHRIHVEKFFSVROCSSIPSPVSGCKETFNLYYEADPDSATKTFPMMEHP 134
 121 WVKVDTIADESFQVDLGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 180
 135 WVKVDTIADESFQVDLGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 194
 181 RKCPRILQNGAIFQETLHSGAESTSLVAARSGCIANAEVDVDPKLYCNGDGMVPIGRC 240
 195 RKCPRILQNGAIFQETLHSGAESTSLVAARSGCIANAEVDVDPKLYCNGDGMVPIGRC 254
 241 MCKAGFAVNGVGVCGCPGCTFKANOGDEACTHCHINSRTTSEGATNCVCRNGYRADL 300
 255 MCKAGFAVNGVGVCGCPGCTFKANOGDEACTHCHINSRTTSEGATNCVCRNGYRADL 314
 301 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGRDLVYNIICSCSGGRACR 360
 315 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGRDLVYNIICSCSGGRACR 374
 361 CGDNVQYAPRQGLGTERIRYISDLAHTOYTFEIOAVNGVTDOSPSPQFASVNIITNQA 420
 375 CGDNVQYAPRQGLGTERIRYISDLAHTOYTFEIOAVNGVTDOSPSPQFASVNIITNQA 434

Qy	421	APSAVSTIMHOVSRIVSDITLSMSQDPQNGVILDELOYENKELSEYNATAIKSPNTVT	480
Db	435	APSAVSTIMHOVSRIVSDITLSMSQDPQNGVILDELOYENKELSEYNATAIKSPNTVT	494
Qy	481	--GKAGAIYVFQVRAATVAGVGRYSGKKYRPTMTAEATYQNSIQEKLPLITGSSAGLV	538
Db	495	VQGLKAGAIYVFQVRAATVAGVGRYSGKKYRPTMTAEATYQNSIQEKLPLITGSSAGLV	554
Qy	539	LIAVVAIATVCNRRGFERADSEYTDKLOHYTSGHITTPGMKIYIDPTVEDPNEAVREFAK	598
Db	555	LIAVVAIATVCNRRGFERADSEYTDKLOHYTSGHITTPGMKIYIDPTVEDPNEAVREFAK	614
Qy	599	EIDISCKIEIOVIGAGEFEGEVCSGHLXILPGKRETFVAIKTISKGYTEKORRDLSEASIN	658
Db	615	EIDISCKIEIOVIGAGEFEGEVCSGHLXILPGKRETFVAIKTISKGYTEKORRDLSEASIN	674
Qy	659	GQPDHPVYHLEGVYTKSPVMIITEFENENSLDSFLRONDQGPVTYQLGMGRGIAAG	718
Db	675	GQPDHPVYHLEGVYTKSPVMIITEFENENSLDSFLRONDQGPVTYQLGMGRGIAAG	734
Qy	719	KYLADNMVYHRLAARNTILVNSLNCXKSDSGSLRFLLEDTSPTTYSALGKFPIRMWA	778
Db	735	KYLADNMVYHRLAARNTILVNSLNCXKSDSGSLRFLLEDTSPTTYSALGKFPIRMWA	794
Qy	779	PEAIQYRKTTASASDVSYGIYVMEVMSYGERPYDMTNOVINAIRQDYLRLPPMDCSA	838
Db	795	PEAIQYRKTTASASDVSYGIYVMEVMSYGERPYDMTNOVINAIRQDYLRLPPMDCSA	854
Qy	839	LHQMLDCCQKQRNRNRPKFGQIVMTLQKMTIRNPSLKAAMPSSGINTPLDLRTTPDYS	898
Db	855	LHQMLDCCQKQRNRNRPKFGQIVMTLQKMTIRNPSLKAAMPSSGINTPLDLRTTPDYS	914
Qy	899	FNTVDEWLTAIKMGQYKESFANAGFTSFQVVSQMMMEDILRVGVTLAGHQKILNSIOM	958
Db	915	FNTVDEWLTAIKMGQYKESFANAGFTSFQVVSQMMMEDILRVGVTLAGHQKILNSIOM	974
Qy	959	RAQNMQIOSVE 969	
Db	975	RAQNMQIOSVE 985	
RESULT 2			
EPB2_MOUSE			
ID	EPB2_MOUSE	STANDARD:	PRT: 993 AA.
AC	P54763: 062213:		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	EPHIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN		
DE	KINASE RECEPTOR EPH-3) (NUK) (SEK-3) (FRAGMENT).		
GN	EPH2 OR EPH3 OR NUK OR SEK3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	Henkemeyer M.;		
RL	Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.		
RL	[2]		
RP	SEQUENCE OF 515-993 FROM N.A.		
RP	STRAIN-BALB/C; TISSUE-Brain;		
RK	MEDLINE=95034306; PubMed=7947319;		
RA	Becker N., Seltanidou T., Murphy P., Mattel M.-G., Topilko P.,		
RA	Meoto A., Wilkinson D.G., Charney P., Gizard P.;		
RT	"Several receptor tyrosine kinase genes of the Eph family are		
RT	genetically expressed in the developing hindbrain.";		
RL	Mech. Dev. 47:3-17(1994).		
RP	FUNCTION:		
RK	MEDLINE=20171264; PubMed=10704386;		
RA	Imondi R., Wideman C., Kaprielian Z.;		
RT	"Complementary expression of transmembrane ephrins and their receptors		

```
RT      in the mouse spinal cord: a possible role in constraining the
RL      orientation of longitudinally projecting axons."
CC      -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. CAN
CC      OPIC DISK EVEN LACKING ITS TYROSINE KINASE DOMAIN. THE LIGAND-
CC      ACTIVATED FORM INTERACTS WITH MULTIPLE PROTEINS, INCLUDING GTPASE-
CC      EPHB2 THROUGH THE JUXTAMEMBRANE TYROSINES RESIDUES (BY
CC      SIMILARITY).
CC      CC
CC      -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE ~ ADP +
CC      PROTEIN TYROSINE PHOSPHATE .
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN CELLS OF THE DEVELOPING OUTER
CC      RETINA.
CC      CC
CC      -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC      -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC      -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRAIN
CC      RECEPTOR SUBFAMILY.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC      or send an email to license@isb-slb.ch) .
CC      -----
DR      EMBL; L28909; AAA72411.1; ALT_INIT.
DR      HSP: X76011; CAA53598.1; -.
DR      MGD; MG1:99611; Ephb2.
DR      InterPro: IPRO00561; -.
DR      InterPro: IPRO00719; -.
DR      InterPro: IPRO01090; -.
DR      InterPro: IPRO01245; -.
DR      InterPro: IPRO01426; -.
DR      InterPro: IPRO01660; -.
DR      InterPro: IPRO01777; -.
DR      Pfam: PF01404; Eph_Ibd; 1.
DR      Pfam: PF00536; SAM; 1.
DR      Pfam: PF00041; fn3_2; 2.
DR      Pfam: PF00069; pk_nase; 1.
DR      ProSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR      ProSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR      ProSITE: PS50011; PROTEIN_KINASE_DOM_1.
DR      ProSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR      ProSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR      ProSITE: PS01186; EGFR_2; UNKNOWN 1.
KW      Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KM      Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT      FT NON_TER          1              1
FT      SIGNAL             <1            25
FT      CHAIN              26            993
FT      DOMAIN             26            550
FT      TRANSMEM           551            571
FT      DOMAIN             572            993
FT      DOMAIN             191            328
FT      DOMAIN             329            438
FT      DOMAIN             439            536
FT      DOMAIN             628            891
FT      DOMAIN             918            993
FT      SITE               991            993
FT      NP_BIND            634            642
FT      BINDING            660            660
FT      ACET_SITE          753            753
FT      MOD_RES            603            603
FT      MOD_RES            609            609
FT      MOD_RES            787            787
FT      MOD_RES            937            937
FT      CARBOHYD           342            343
FT      CARBOHYD           435            435
FT      CARBOHYD           435            435
```

FT CARBOHYD 489 489 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 575 575 R-> RR (IN REF. 2).
 SO SEQUENCE 993 AA: 110628 MW: A0E1A695F46587E8 CRC64;

Query Match 99.3%; Score 5082; DB 1; Length 993;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 1 LLAAVEETLMDSTTAAELGMVHPSPGNEEVSGETDENMNTIRTYOVCAVNESSNNMLR 60
 DB 22 LLAAVEETLMDSTTAAELGMVHPSPGNEEVSGETDENMNTIRTYOVCAVNESSNNMLR 81
 QY 61 TKIRRRGARHIVEMKFSVRCOSSIPSPGCKETENLYTEADPFDSATKTFPMWMEHP 120
 DB 82 TKIRRRGARHIVEMKFSVRCOSSIPSPGCKETENLYTEADPFDSATKTFPMWMEHP 141
 QY 121 WVKVDTIADESFOYDLGGRVAKINTEVRSFGPVSRSGFYLAPODYGGCMLIAVRFY 180
 DB 142 WVKVDTIADESFOYDLGGRVAKINTEVRSFGPVSRSGFYLAPODYGGCMLIAVRFY 201
 QY 181 RKCPRITQNCATFOETLSCAESTSLVAARGSCITANAEVDVPIKLYCNGDGEMLVIGRC 240
 DB 202 RKCPRITQNCATFOETLSCAESTSLVAARGSCITANAEVDVPIKLYCNGDGEMLVIGRC 261
 QY 241 MCRAGFEAVNGTFCRCGPGSTFKANGDEACTHCPINSTRTSEGATNCVRNGYRADL 300
 DB 262 MCRAGFEAVNGTFCRCGPGSTFKANGDEACTHCPINSTRTSEGATNCVRNGYRADL 321
 QY 301 DPLDMPCTTIPSAFOAVISSVNETSLMLEWTPPRDSGREDLYNNITICSGSGRACR 360
 DB 322 DPLDMPCTTIPSAFOAVISSVNETSLMLEWTPPRDSGREDLYNNITICSGSGRACR 381
 QY 361 CGDMVOYAPRQGLTEPRITYSDLAHTQYTFEIOAVNGYTDOSPSPASVNIITNOA 420
 DB 382 CGDMVOYAPRQGLTEPRITYSDLAHTQYTFEIOAVNGYTDOSPSPASVNIITNOA 441
 QY 421 APSAVSIMHOVSRTVDSTLTSWSPDPDPNGYILDYELQYKEKELSEVNAATKSPNTVT 480
 DB 442 APSAVSIMHOVSRTVDSTLTSWSPDPDPNGYILDYELQYKEKELSEVNAATKSPNTVT 501
 QY 481 -GKAGAIYFOYARARIVAGYGRYSGKMYFQMTAEAYQTSIOEKLPLIIGSSAGLVF 538
 DB 502 VQGLKAGAIYFOYARARIVAGYGRYSGKMYFQMTAEAYQTSIOEKLPLIIGSSAGLVF 561
 QY 539 LIAVVVIAIVCNRGFEERADSEYTDKIQHTSGHITFGMKIYIDPFYEDPNEAVREFAK 598
 DB 561 LIAVVVIAIVCNRGFEERADSEYTDKIQHTSGHITFGMKIYIDPFYEDPNEAVREFAK 621
 QY 599 EIDISCVRIEYIAGGEGEVCOSGHLKPGKREIFVAIKTLKSGTEKORRDFLSEASIM 658
 DB 622 EIDISCVRIEYIAGGEGEVCOSGHLKPGKREIFVAIKTLKSGTEKORRDFLSEASIM 681
 QY 659 GGFDPBNVTHLEGVVTKSTPVMIITEFEMENGLSDFLRQNDGQFTVIQVLMKRGIAAGM 718
 DB 682 GGFDPBNVTHLEGVVTKSTPVMIITEFEMENGLSDFLRQNDGQFTVIQVLMKRGIAAGM 741
 QY 719 KTLADNIVHRLAARNILVNSNLVCKYSDFGLSRFLSDDPITSDPYTALGKPIRMTA 778
 DB 742 KTLADNIVHRLAARNILVNSNLVCKYSDFGLSRFLSDDPITSDPYTALGKPIRMTA 801
 QY 779 PEAIOYRKFTSADVWSYGIYVMEVWSYGERPYMDTNDVINAIEODYRLPPMDCSA 838
 DB 802 PEAIOYRKFTSADVWSYGIYVMEVWSYGERPYMDTNDVINAIEODYRLPPMDCSA 861
 QY 839 LHLQMLDCQOKRNRHPRFGQIVNTLDMKIRNPNSIKAMAPLSSSGINLPILDRTIPDYS 898
 DB 862 LHLQMLDCQOKRNRHPRFGQIVNTLDMKIRNPNSIKAMAPLSSSGINLPILDRTIPDYS 921
 QY 899 FNTVDDEMLAIKMGQYKESFANAGTSPDVVSOMMEDILRIGVTLTAGHOKKILNSIOVM 958
 DB 922 FNTVDDEMLAIKMGQYKESFANAGTSPDVVSOMMEDILRIGVTLTAGHOKKILNSIOVM 981

QY 959 RAOMNOIOSVEV 970
 DB 982 RAOMNOIOSVEV 993

RESULT 3
 EPH2_CHICK ID EPH2_CHICK STANDARD; PRT: 1004 AA.
 AC P28693;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-OCT-2000 (Rel. 40, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK5).
 GN EPHB2 OR CEK5.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RC TISSUE=Embryo;
 RX MEDLINE=92144672; PubMed=1664238;
 RA Pasquale E.B.;
 RT Identification of chicken embryo kinase 5, a developmentally regulated receptor-type tyrosine kinase of the Eph family.";
 RL Cell Regul. 2:523-534(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RC TISSUE=Brain;
 RX MEDLINE=93288394; PubMed=8510926;
 RA Sajjadi F.G., Pasquale E.B.;
 RT "Five novel avian Eph-related tyrosine kinases are differentially expressed".
 RL Oncogene 8:1807-1813(1993).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. PROBABLY AN IMPORTANT COMPONENT OF SIGNAL TRANSDUCTION PATHWAYS.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM/CEK5+ (SHOWN HERE) AND A SHORT FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION THROUGHOUT DEVELOPMENT AND SPECIFICALLY EXPRESSED IN THE CENTRAL NERVOUS SYSTEM.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M62325; AAA48667.1; ALT_INIT.
 CC HSSP: P00523; 2PTK.
 DR InterPro: IPR000561;
 DR InterPro: IPR000719;
 DR InterPro: IPR001090;
 DR InterPro: IPR001245;
 DR InterPro: IPR001426;
 DR InterPro: IPR001660;
 DR InterPro: IPR001777;
 DR Pfam: PF01404; EPH_1bd; 1.
 DR Pfam: PF00536; SAM_1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.

DR PRINTS: PRO00104; ENTPEP11.
 DR PROSITE: PRO0107; TYRKINASE.
 DR PROSITE: PS00109; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_DOM_1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1_1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2_1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
 KW Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 1004 EPHRIN TYPE-B RECEPTOR 2.
 FT DOMAIN 20 544 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 545 565 POTENTIAL.
 FT DOMAIN 566 1004 CYTOSOLASMIC (POTENTIAL).
 FT DOMAIN 20 321 CYS-RICH.
 FT DOMAIN 326 419 FIBRONECTIN TYPE-III.
 FT DOMAIN 437 521 FIBRONECTIN TYPE-III.
 FT DOMAIN 639 902 PROTEIN KINASE.
 FT DOMAIN 929 1004 SAM.
 FT SITE 1002 1004 PDZ-BINDING MOTIF (POTENTIAL).
 FT NP_BIND 645 653 ATP (BY SIMILARITY).
 FT BINDING 671 671 ATP (BY SIMILARITY).
 FT ACT_SITE 764 764 BY SIMILARITY.
 FT MOD_RES 614 614 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 620 620 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 798 798 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 948 948 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPIC 591 606 MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 1004 AA; 111963 MW; 8D26213970ECC6D CnC64.

Query Match Best Local Similarity 96.48; Score 4932.5; DB 1; Length 1004;
 Matches 930; Conservative 28; Mismatches 12; Indels 19; Gaps 3;

QY 1 LLAVEETLMDSTATATLALGMVHPPSGMEVSGYDENMNTIRYOCNPESSONMLR 60
 D 16 LLAVEETLMDSTATATLALGMVHPPSGMEVSGYDENMNTIRYOCNPESSONMLR 75
 QY 61 TKETRRRGARHRIHEMKEFSVYDCSSIPSPGCKETENLYYEADFPDPAKTFPPNMENP 120
 D 76 TKETRRRGARHRIHEMKEFSVYDCSSIPSPGCKETENLYYEADFPDPAKTFPPNMENP 135
 QY 121 WVKVDTAADSFSQVLDGKVMKINTEVSGVSGYSLAFODYGCMSLIAVREY 180
 D 136 WVKVDTAADSFSQVLDGKVMKINTEVSGVSGYSLAFODYGCMSLIAVREY 195
 QY 181 RKPRIQNGAIFQETLSGAESTSLVAARGSCINAEVNPVILYNGSGEMVPIGRC 240
 D 196 RKPRIQNGAIFQETLSGAESTSLVAARGSCINAEVNPVILYNGSGEMVPIGRC 255
 QY 241 MCKAGFAVENGVYCRGCPGSGTFKANGDCACTHCPINSTRTSGATNCVCNNGYRADL 300
 D 256 MCKAGFAVENGVYCRGCPGSGTFKANGDCACTHCPINSTRTSGATNCVCNNGYRADL 315
 QY 301 DPLDMPCTTIPSAPOAVISSVNEISLMEWTPRPSDGSGRDLYNITCKSCGSGRACATR 360
 D 316 DPLDMPCTTIPSAPOAVISSVNEISLMEWTPRPSDGSGRDLYNITCKSCGSGRACATR 375
 QY 361 CGDNVQAPRQGLTEPRIRIISDLAHTQYTFEIOANGVTDDSPSPASVINITTNOA 420
 D 376 CGDNVQAPRQGLTEPRIRIISDLAHTQYTFEIOANGVTDDSPSPASVINITTNOA 435
 QY 421 APSAVSITMHOVSRTVDSTLSSQSPDQPNGVILDELYEYKELSEYNATAIKSPNTTV 480
 D 436 APSAVSITMHOVSRTVDSTLSSQSPDQPNGVILDELYEYKELSEYNATAIKSPNTTV 495

QY 481 --GLKAGAIYFQVARTVAGYGRYSGMYFOTTEAEYOTSIOEKLPLIISSAACTV 538
 D 496 VQNKAGAIYFQVARTVAGYGRYSGMYFOTTEAEYOTSIOEKLPLIISSAACTV 555
 QY 539 LIAVVAIVACN -RRGERADSEYTKLQHTSGH-----ITPGMKIYI 581
 D 556 LIAVVAIVACN -RRGERADSEYTKLQHTSGH-----ITPGMKIYI 615
 QY 582 DPEFYEDPNEAVREFAEIDISCKIIOVIGAGFEGVCGHLKPKREIFAIAKTLKS 641
 D 616 DPEFYEDPNEAVREFAEIDISCKIIOVIGAGFEGVCGHLKPKREIFAIAKTLKS 675
 QY 642 GYTEKQRDEISEASINGQFDHPVHILLEGVTKSTPYMTITEPMENGLSDSFLRNDGO 701
 D 676 GYTEKQRDEISEASINGQFDHPVHILLEGVTKSTPYMTITEPMENGLSDSFLRNDGO 735
 QY 702 FTVYQLVGMRLGIAAGKKYLAADNMYVRDLAARNIILVNSLVCKVSPDGLSRLLEDOTSD 761
 D 736 FTVYQLVGMRLGIAAGKKYLAADNMYVRDLAARNIILVNSLVCKVSPDGLSRLLEDOTSD 795
 QY 762 PTVYSAIGKFPRTWTAPEAIQYRKFTSASDVMSYGIYVMEVNSYGERPYMDTNDVYN 821
 D 796 PTVYSAIGKFPRTWTAPEAIQYRKFTSASDVMSYGIYVMEVNSYGERPYMDTNDVYN 855
 QY 822 AIEODYRLPPMDCPSALHOLMLDCMOKDRNHRPKFGQIVNTLDKMI RNPSLKAMAPLS 881
 D 856 AIEODYRLPPMDCPSALHOLMLDCMOKDRNHRPKFGQIVNTLDKMI RNPSLKAMAPLS 915
 QY 882 SGINPLDRTIDYTSFNTVDLEIAIKMGQYKESFANAGFTSPVDSQMMEDILRVG 941
 D 916 SGINPLDRTIDYTSFNTVDLEIAIKMGQYKESFANAGFTSPVDSQMMEDILRVG 975
 QY 942 VTLAAGHOKITLNSIOVRAQMOIOSEYV 970
 D 976 VTLAAGHOKITLNSIOVRAQMOIOSEYV 1004

RESULT 4
 ID EPH2_COTUA STANDARD; PRT; 987 AA.
 AC 090344;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR GEF5).
 GN EPHB2 OR GEF5.
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 OX NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA MEDLINE=96109331; PubMed=8612986;
 RX Kenny D., Bronner-Fraser M., Marcelle C.;
 RT "The receptor tyrosine kinase GEF5 mRNA is expressed in a gradient
 RT within the neural retina and the tectum.";
 RL Dev. Biol. 172:708-716(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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CC EMBL: X91737; CA62862.1; -
 DR HSPB; P00523; 2PK.
 DR InterPro: IPR000561; -
 DR InterPro: IPR000719; -
 DR InterPro: IPR001090; -
 DR InterPro: IPR001245; -
 DR InterPro: IPR001426; -
 DR InterPro: IPR001660; -
 DR InterPro: IPR001777; -
 DR Pfam: PF01404; EPH_Lbd; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00014; ENTRYPERIT.
 DR PRINTS: PR00109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; FALSE_NEG.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR Transferrase: Tyrosine-protein kinase: ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 19
 FT CHAIN 20 987
 FT DOMAIN 20 544
 FT TRAMEM 545 565
 FT DOMAIN 566 987
 FT DOMAIN 185 322
 FT DOMAIN 323 432
 FT DOMAIN 433 530
 FT DOMAIN 530 885
 FT DOMAIN 912 987
 FT SITE 987 987
 FT NP_BIND 628 636
 FT BINDING 654 654
 FT ACT_SITE 747 747
 FT MOD_RES 597 597
 FT MOD_RES 603 603
 FT MOD_RES 781 781
 FT MOD_RES 931 931
 FT CARBOHYD 266 266
 FT CARBOHYD 337 337
 FT CARBOHYD 429 429
 FT CARBOHYD 478 478
 FT CARBOHYD 483 483
 SQ SEQUENCE 987 AA; 110331 MW; 05D6ECC68B718DD7 CRC64;

Query Match 95.8%; Score 4902; DB 1; Length 987;
 Best Local Similarity 94.7%; Pred. No. 1e-295;
 Matches 920; Conservative 30; Mismatches 20; Indels 2; Gaps 1;

QY 1 LLAAVEETLMDSTTATTAELGMMVPPSGMEVSGYDENMNTITTYOVCAVFESSQNNMLR 60
 DB 16 LLAAVEETLMDSTTATTAELGMMVPPSGMEVSGYDENMNTITTYOVCAVFESSQNNMLR 75
 QY 61 TKIIRRGARIRIVEMKFSVRDCSSIPNPGSKETFNLYYSDDSDAKTTPNMNEN 120
 DB 76 TKIIRRGARIRIVEMKFSVRDCSSIPNPGSKETFNLYYSDDSDAKTTPNMNEN 135
 QY 121 WYVYDTIADESFQYDGLGRVAKINTEVRSFGVSRSGFYLAFODYGGCMLIAVRVF 180
 DB 136 WYVYDTIADESFQYDGLGRVAKINTEVRSFGVSRSGFYLAFODYGGCMLIAVRVF 195
 QY 181 RKPRIIONCAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYONGDEWLVPIGRC 240
 DB 196 RKPRIIONCAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYONGDEWLVPIGRC 255

QY 241 MCKAGFEAVENGTCRGCGSGTFRKANGDEACTHCPINSRTTSGATNCYCRRNGYRADL 300
 DB 256 MCKAGFEAVENGTCRGCGSGTFRKANGDEACTHCPINSRTTSGATNCYCRRNGYRADL 315
 QY 301 DPLDMPCTTIPSAPOAVASSVNETSLMELWTPPRDSGGREDLVYNIICKSGSGRGACTR 360
 DB 316 DPLDMPCTTIPSAPOAVASSVNETSLMELWTPPRDSGGREDLVYNIICKSGSGRGACTR 375
 QY 361 CGDNVQVAPROLGLTEPRITYISDLARIQYTFEIQAVNGVTDOSPSPQPSVNTITNOA 420
 DB 376 CGDNVQVAPROLGLTEPRITYISDLARIQYTFEIQAVNGVTDOSPSPQPSVNTITNOA 435
 QY 421 APSAIVIMHOVSRFVDSFTLSMSOPDPONGYILDELOYEKESEYNATAIKSPNTVT 480
 DB 436 APSAIVIMHOVSRFVDSFTLSMSOPDPONGYILDELOYEKESEYNATAIKSPNTVT 495
 QY 481 --GLKAGAIYFOVARTVAGYGRYSGRMYPQMTAEYQTSIOEKLPLIIGSSAGLVE 538
 DB 496 --GLKAGAIYFOVARTVAGYGRYSGRMYPQMTAEYQTSIOEKLPLIIGSSAGLVE 555
 QY 539 LIAVYVIAVCNRKGEERADSEYTDKLOHTSGHTPGMKTYIDPTEYEDNEAVREFAK 598
 DB 556 LIAVYVIAVCNRKGEERADSEYTDKLOHTSGHTPGMKTYIDPTEYEDNEAVREFAK 615
 QY 599 EIDISCVKIEQYIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDPLSEASIM 658
 DB 616 EIDISCVKIEQYIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDPLSEASIM 675
 QY 659 GGFDPHNVIAHLEGVTKSTPVMTITEPMENGLSDSFLQNDGQFVIOVGMKGIAGM 718
 DB 676 GGFDPHNVIAHLEGVTKSTPVMTITEPMENGLSDSFLQNDGQFVIOVGMKGIAGM 735
 QY 719 KYLAAMNVYHRLAFLNLTIVNSNLCKVSDGLSFLBDDTSDPYTTSALGKPIRMTA 778
 DB 736 KYLAAMNVYHRLAFLNLTIVNSNLCKVSDGLSFLBDDTSDPYTTSALGKPIRMTA 795
 QY 779 PEAIORRFTSASDVYSYGIWMEVMSYGERPYMDTNOVYINAEODYRLPPMDCSA 838
 DB 796 PEAIORRFTSASDVYSYGIWMEVMSYGERPYMDTNOVYINAEODYRLPPMDCSA 855
 QY 839 LHQMLDCQKDRNHPEKFGQIVNTLDMKIRPNLSLKMAAPLSSGINPLDRTIPDYS 898
 DB 856 LHQMLDCQKDRNHPEKFGQIVNTLDMKIRPNLSLKMAAPLSSGINPLDRTIPDYS 915
 QY 899 ENTVEEMLEATIMGOYKESFANAGTSPDYVSQMMEDILIRGVYTLAGHOKKILINSIQM 958
 DB 916 ENTVEEMLEATIMGOYKESFANAGTSPDYVSQMMEDILIRGVYTLAGHOKKILINSIQM 975
 QY 959 RAQMNOIOSVEV 970
 DB 976 RAQMNOIOSVEV 987

RESULT 5
 EEBL_RAT STANDARD; PRT; 984 AA.
 ID EEBL_RAT
 AC P09759;
 DT 01-MAR-1989 (rel. 10, created)
 DT 01-DEC-1992 (rel. 24, last sequence update)
 DT 01-OCT-2000 (rel. 40, last annotation update)
 DE EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (BC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EPH-2) (ELK).
 GN EPHB1 OR EPHB2 OR ELK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX MEDLINE=91203869; PubMed=2017163;
 Lhotak V., Greer P., Letwin K., Pawson T.;

RT "Characterization of elk, a brain-specific receptor tyrosine kinase."
 RL Mol. Cell. Biol. 11:2496-2502(1991).
 RN [2]
 RP SEQUENCE OF 605-984 FROM N.A.
 RC STRAIN-MISTAR: TISSUE-Brain:
 RX MEDLINE-94167102; PubMed-2465255;
 RA Letwin K., Yee S.P., Pawson T.;
 RT "Novel protein-tyrosine kinase cdnas related to fps/fes and eph cloned
 using anti-phosphotyrosine antibody."
 RL Oncogene 3:621-627(1988).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
 EPHRIN-B1, -B2 AND -B3. MAY BE INVOLVED IN CELL-CELL INTERACTIONS
 IN THE NERVOUS SYSTEM.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBUNIT: THE LIGAND-ACTIVATED FORM INTERACTS WITH GRB2, GRB10 AND
 NCK THROUGH THEIR RESPECTIVE SH2 DOMAINS. THE GRB10 SH2 DOMAIN
 BINDS EPHB1 THROUGH TYR-928. WHILE GRB2 BINDS RESIDUES WITHIN THE
 CATALYTIC DOMAIN. THE NCK SH2 DOMAIN BINDS EPHB1 THROUGH TYR-594.
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO BRAIN AND TESTES.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC RECEPTOR SUBFAMILY
 CC -----
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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M59814; -; NOT_ANNOTATED_CDS.
 DR EMBL: X13411; CA3177.1; -;
 DR PIR: S04327; S04327.
 DR PIR: A39753; A39753.
 DR HSP: P00523; 2PTK.
 DR InterPro: IPR000561; -;
 DR InterPro: IPR000719; -;
 DR InterPro: IPR001090; -;
 DR InterPro: IPR001245; -;
 DR InterPro: IPR001426; -;
 DR InterPro: IPR001660; -;
 DR InterPro: IPR001777; -;
 DR Pfam: PF01404; BPH_1bd; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PRO0014; FNTYPEIIT.
 DR PRINTS: PRO0109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN; 1.
 DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 17
 FT CHAIN 1 984
 FT DOMAIN 18 984
 FT TRANSSEM 541 563
 FT DOMAIN 541 563
 FT DOMAIN 564 984
 FT DOMAIN 183 319
 FT DOMAIN 320 429
 FT DOMAIN 430 527
 FT DOMAIN 619 882
 FT DOMAIN 909 984
 FT SITE 982 984
 FT NF_BIND 625 633
 ATP (BY SIMILARITY).

FT BINDING 651 651 ATP (BY SIMILARITY).
 FT ACT_SITE 744 744
 FT MOD_RES 594 594 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 600 600 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 778 778 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 928 928 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 426 426 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 480 480 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 984 AA; 109882 MW; 521EAC4008BF91A CRC64;
 Query Match 76.5% Score 3914.5; DB 1; Length 984;
 Best Local Similarity 74.0% Pred. No. 1.2e-234;
 Matches 711; Conservative 128; Mismatches 121; Indels 3; Gaps 2;
 QY 2 LAAVEETLMSTATAETAEIGMNVHPGSGMEESGVDENMTIRYOVNVESSONMRLT 61
 DB 15 VAAMEETLMDTRTATETAEIGMNVHPGSGMEESGVDENMTIRYOVNVESSONMRLT 74
 QY 62 KETRRGAHRIHVEKTSVNDCCSIPSPGCKETENLYYEADFDPSATKTFPMNENPM 121
 DB 75 TETRRGAHRIHVEKTSVNDCCSIPSPGCKETENLYYEADFDPSATKTFPMNENPM 134
 QY 122 VKVDIADESEFSOVDLGGHVMKINTEVRSRGPVSRSGFLAODYGGCSLIAVVEPR 181
 DB 135 LKVDIADESEFSOVDLGGHVMKINTEVRSRGPVSRSGFLAODYGGCSLIAVVEPR 194
 QY 182 KCPPIONGAIFDETSAGBSTSLVAARGSIANAEEVDPIKLYCNGDEMLVPIGRCM 241
 DB 195 KCPPIYONFAVPEETMGASTSLVIARGICPINAEEVDPIKLYCNGDEMLVPIGRCT 254
 QY 242 CKAGFEAVENGTCRGPGSGTEKANGDEACTHCPIINSRTSGATNCVCRNGYRADLD 301
 DB 255 CKAGYEP-ENSVACKACPACTFKASQAEBSCHSPSSPSASPICICRNGYRADLD 313
 QY 302 PLDMCTTPSAPQAVISSVNETSLMEWTPPRDSGRDVLVNIICKSGSGRGCTRC 361
 DB 314 PPEVACTVPSGPRNVISYIENETSLMEHPREITGRDVTYNIICKCRADRSCSCNC 373
 QY 362 GDNVOYAPRDLGLTEPRITISDLATYTFELQAVNGVTDSPSPQFASVNTTNOA 421
 DB 374 DDNVEFVPRLGLTEPRISLISLMAHPYTFDQANGVSSSPPEQHVSVNTTNOA 433
 QY 422 PSAVSIMHOVSRTVDSITLSMSPQDPNGVITLDELOYEKELSEYNATKISPTNT--V 479
 DB 434 PSTVPIHGOVSATMRISITLSMSPQDPNGVITLDELOYEKELSEYNATKISPTNT 493
 QY 480 TGLKACAIYFOVARTAVAGYRGYSKMYEQMTAEVOTSIOERLPLITIGSSAGLVFL 539
 DB 494 DGLRPGMVYVVOVRATVAGYRGYSKMYEQMTAEVOTSIOERLPLITIGSSAGLVFL 553
 QY 540 IAVVVAIYCNRRGEFRAASEYTDKLOHTSGHTIPGKIYIDPTTYEDPNEAVERKE 599
 DB 554 VSLVAISTYCKSKRAYSKRAYISDKLOHTSGRSGPGKIYIDPTTYEDPNEAVERKE 613
 QY 600 IDISCVKIEOVYIAGEFEVSGHGLPKGREIFAVALITLKSQTEKOROPFLSPASTG 659
 DB 614 IDVSEFKIEEVYIAGEFEVSGHGLPKGREIFAVALITLKSQTEKOROPFLSPASTG 673
 QY 660 OPDHNVIHLEGVYKSPVMAITTEFMNGSLDPLRONDQCFYVIOLVGLRIGIAGMK 719
 DB 674 OPDHNVIHLEGVYKSPVMAITTEFMNGSLDPLRONDQCFYVIOLVGLRIGIAGMK 733
 QY 720 YLADNNVYHRLAARINILVNSNLCKYVDFGLSPRLLEDOTSDPTYSLLGKKPIRTAP 779
 DB 734 YLSENNVYHRLAARINILVNSNLCKYVDFGLSPRLLEDOTSDPTYSLLGKKPIRTAP 793
 QY 780 EAIQVKTTSASDVWSGIVMEVWSYGERPYMDTNOVINAIEDORYRLPAPPDCSAL 839
 DB 794 EAIARKTTSASDVWSGIVMEVWSYGERPYMDTNOVINAIEDORYRLPAPPDCSAL 853
 QY 840 HOLMDCWQKQRNRRPKRGQIVNTLDMKIRNPNSLKMAAPLSSGINTLPLDRTIIPDYTSF 899

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DB 854 HOLMLDCKOKDNRSPRFRFVINTLDMKIMRNPSLKTATVATVAVSOPDLRSPIDFTAF 913
OY 900 NTVDWELAIKMGQYKESFANAGFTSPDYVSCMMEDIRVAVTAGIOKILNIOYMR 959
DB 914 TVYDWMLSAIKMYQYRDSFLTAGFTSLQVWQMSDELLRIGVLAGHOKILTSISHSR 973
OY 960 AQMNQOSV 968
DB 974 VQMNOSPSV 982

RESULT 6
EPH1_HUMAN STANDARD: PRT: 984 AA.
ID EPB1_HUMAN
AC P54762; 043569; 095142; 095143;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
KINASE RECEPTOR EPH-2) (NET) (HEK6) (ELK).
GN EPHB1 OR EPH2 OR NET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_Taxid=9606;
OX [1]
RN SEQUENCE FROM N.A. (ISOFORM EPHB1A).
RC TISSUE=Fetal brain;
RA MEDLINE=96115594; PubMed=8666391;
RA Tang X.X., Biegel J.A., Nycum L.M., Yoshioka A., Brodeur G.M.,
RA Pleasure D.E., Ikegaki N.;
RT "DNA cloning, molecular characterization, and chromosomal
RT localization of NET(EPH2), a human EPH-related receptor protein-
RT tyrosine kinase gene preferentially expressed in brain.";
RL Genomics 29:426-437(1995).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORMS EPHB1A TO EPHB1D).
RC TISSUE=Kidney;
RA Stein E., Schoeckmann H.O., Daniel T.O.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RN INTERACTIONS WITH GRB2 AND GRB10.
RA MEDLINE=96394464; PubMed=8798570;
RA Stein E., Cerretti D.P., Daniel T.O.;
RT "Ligand activation of ELK receptor tyrosine kinase promotes its
RT association with Grb10 and Grb2 in vascular endothelial cells.";
RL J. Biol. Chem. 271:23568-23593(1996).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
CC EPHRIN-B1, -B2 AND -B3. MAY BE INVOLVED IN CELL-CELL INTERACTIONS
CC IN THE NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBUNIT: THE LIGAND-ACTIVATED FORM INTERACTS WITH GRB2, GRB10 AND
CC NCK THROUGH THEIR RESPECTIVE SH2 DOMAINS. THE GRB10 SH2 DOMAIN
CC BINDS EPHB1 THROUGH TYR-928, WHILE GRB2 BINDS RESIDUES WITHIN THE
CC CATALYTIC DOMAIN. THE NCK SH2 DOMAIN BINDS EPHB1 THROUGH TYR-594.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS, EPHB1A (SHOWN HERE), EPHB1B,
CC EPHB1C AND EPHB1D; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN BRAIN.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC EMBL: L40636; AAB08520.1; -
DR EMBL: AF037331; AAD02030.1; -
DR EMBL: AF037332; AAD02031.1; -
DR EMBL: AF037333; AAB94627.1; -
DR EMBL: AF037334; AAB94628.1; -
DR HSP: P00523; 2PTK.
DR MIM: 600600; -
DR InterPro: IPR000561; -
DR InterPro: IPR000719; -
DR InterPro: IPR001090; -
DR InterPro: IPR001245; -
DR InterPro: IPR001426; -
DR InterPro: IPR001660; -
DR InterPro: IPR001777; -
DR Pfam: PF01404; EPH_lbd1.1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00014; FNTYPEIIL.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN; 1.
KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 17
FT CHAIN 18 984
FT DOMAIN 18 540
FT TRANSMEM 541 563
FT DOMAIN 564 964
FT DOMAIN 183 319
FT DOMAIN 320 429
FT DOMAIN 430 527
FT DOMAIN 619 882
FT DOMAIN 902 984
FT SITE 985 984
FT NP_BIND 625 633
FT BINDING 651 651
FT ACT_SITE 744 744
FT MOD_RES 594 594
FT MOD_RES 600 600
FT MOD_RES 778 778
FT MOD_RES 928 928
FT CARBOHYD 334 334
FT CARBOHYD 426 426
FT CARBOHYD 480 480
FT VARSPPLIC 1 27
FT VARSPPLIC 617 984
FT VARSPPLIC 642 682
FT CONFLICT 12 12
FT CONFLICT 87 37
FT CONFLICT 152 152
FT CONFLICT 185 135
FT CONFLICT 274 274
FT CONFLICT 336 336
FT CONFLICT 367 367
FT CONFLICT 485 485
FT CONFLICT 813 813
FT CONFLICT 819 819
FT CONFLICT 847 847
FT CONFLICT 973 973
FT SQ SEQUENCE 984 AA; 109884 MW; 8044160E24E93A92 CRC64;

Query Match 76.2%; Score 3899.5; DB 1; Length 984;
Best Local Similarity 73.8%; Fred. No. 1e-233;
Matches 712; Conservative 130; Mismatches 120; Indels 3; Gaps 2;

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QY 2 LAABETLMDSTTAAEAGMAYHPSSGMEVSGYDENNNITRTYOVAVPESSONMLRT 61
Db 15 VAAEBETLMDSTTAAEAGMAYHPSSGMEVSGYDENNNITRTYOVAVPESSONMLRT 74
QY 62 KIRRRGAHRIIVEKFFSVBPOSSIPSPGCKEFENLYYEADFDSTKTFPMWENPW 121
Db 75 TFINRGARHRIITEKFTVRCOSSLPNPGCKEFENLYYEADFDSTKTFPMWENPW 134
QY 122 VKVDITIADESEFOVDLGRMYKINTEVRSFPGVSRSGFYLAPODYGCSNLIARVEYR 181
Db 135 LKVDITIADESEFOVDLGRMYKINTEVRSFPGVSRSGFYLAPODYGCSNLIARVEYR 194
QY 182 KCPRTIONGALFOETLSAESTSLVAANGSCITANAEEVDYPIKLYCNGDEMIWPIGRCM 241
Db 195 KCPSTVONFAVPEETMTGAESTSLVANGSCITANAEEVDYPIKLYCNGDEMIWPIGRCT 254
QY 242 CKAGEEAVENGTVRCGSPGTFKKNNOGDEACTHCPINSRTSEATNCVCRNGYRADLD 301
Db 255 CKPGYEP-ENSVACKACAGTFKASQAEKSGHCPSPNSRSPAEASPICTCTGTGYRADFD 313
QY 302 PLDMPTTIPAPAVISSVNETSLMLMTPPRDSGGREDLVYNIICKSGSGGACTRC 361
Db 314 PPEVACTSPSPGPNVSIYNETSIILEMHPRETGRDVTYNIICKGRADRSRC 373
QY 362 GDNVQVAPROGLTEPRITYSDLLAHTOYFETQAVGVTDOSFPOFASVNTTNOA 421
Db 374 DNVNEFPROGLTECHVYSSISLMAHTPYTFDQALNGVSSKSPPOHVSNTTNOA 433
QY 422 PSAVSIMHOVSRTVDSITLMSOPDPONGVILDELOQYKEKELSEYVATAIKSPNT -V 479
Db 434 PSTVPIHVOVSATRSITLSMPDEQNGIILDEIRYKEKELSEYVATAIKSPNT -V 493
QY 480 TGKAGAIYFOVARTVAGYGRSGMAYQTMTEAYQTSIOEKLPLIGSSAGLVFL 539
Db 494 DGLPGVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 553
QY 540 IAVVAVIYVNRKGFERADSEYTDLOHTYSGHITPGMKYIDPTEYEDNEVREAKE 599
Db 554 VSVIAIVSRRKAYSKAVYCDKLOHYSTGSGOMKIYIDPTEYEDNEVREAKE 613
QY 600 IDISCAVIEOVIGAGEFEGVCSGHLKPKGREIFVAIKTLKSGYTERKORDELSEASING 659
Db 614 IDVSFVIEVIGAGEFEGVCSGHLKPKGREIFVAIKTLKAGYSEKORDELSEASING 673
QY 660 QPDHPNTHLEGVVTKSTPVMITTEEMENSILDSFLRONDGOVTYQVLYGMLGIAAGK 719
Db 674 QPDHPNTHLEGVVTKSTPVMITTEEMENGALDSFLRONDGOVTYQVLYGMLGIAAGK 733
QY 720 YLADMYVHRDLAARNILVNSNLVCKVSDGSLRFLDPTSDPTYSALGKFPJRWTP 779
Db 734 YLAEMNVHRDLAARNILVNSNLVCKVSDGSLRFLDPTSDPTYSALGKFPJRWTP 793
QY 780 EAOYKRTFSASVNSYGVIMMEVNSYGERPYWDMTNOVINAIEDYRLPPMDCPSAL 839
Db 794 EALAYKRTFSASVNSYGVIMMEVNSYGERPYWDMTNOVINAIEDYRLPPMDCPSAL 853
QY 840 HOLMLCQOKDRHHRPKFGQIYNTLDKMRBNPNSIKAMAPLSSGINTPLDPTTIDYVSF 899
Db 854 HOLMLCQOKDRHHRPKFGQIYNTLDKMRBNPNSIKAMAPLSSGINTPLDPTTIDYVSF 913
QY 900 NVVDENLEAIKMGQYKESFANAGFTSFVYVSQMMEDILRVGVTLAGHOKKLINSIQWR 959
Db 914 TVYDDMLSAIKMGQYKESFANAGFTSFVYVSQMMEDILRVGVTLAGHOKKLINSIQWR 973
QY 960 AQMNQ 964
Db 974 VOISQ 978

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RESULT 7
EPBA_XENLA
ID EPBA_XENLA STANDARD: PRT: 985 AA.

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AC G91571;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 1A PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR XEK).
GN XEK.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95215070; PubMed=7700636;
RA Jones T.L., Karavanova I., Maeno M., Ong R.C., Kung H.-F., Daar I.O.;
RT "Expression of an amphibian homolog of the Eph family of receptor
RT tyrosine kinases is developmentally regulated."
RL Oncogene 10:1111-1117(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. MAY PLAY A
CC ROLE IN THE DEVELOPMENT OR FUNCTION OF THE CENTRAL NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID
CC BLASTULA TRANSITION AND REAPPEARS AT LATE NEURULATION. EXPRESSED
CC AT HIGHER LEVELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC
CC STAGES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UBQUITOUSLY
CC EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OVARY. EXPRESSION IN
CC THE BRAIN, BRACHIAL ARCHES, TRIGEMINAL FACIAL GANGLION, AND THE
CC RETINA OF SWIMMING TADPOLE STAGE OF DEVELOPMENT.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC -----
DR EMBL: U14164; AA07488.1;
DR HSSP: P00523; 2PTK.
DR InterPro: IPR000719;
DR InterPro: IPR001090;
DR InterPro: IPR001245;
DR InterPro: IPR001426;
DR InterPro: IPR001660;
DR InterPro: IPR001777;
DR InterPro: IPR001899;
DR Pfam: PF001404; EPH_1bd.1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; FALSE_NRG.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 985
FT DOMAIN 20 542
FT TRANSMEM 543 563
FT DOMAIN 564 985
FT DOMAIN 185 321
FT DOMAIN 322 431
FT FIBRONECTIN TYPE-III.

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DR pfam: PF00041; f03; 2.
 DR PROSITE: PS00107; KINASE_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM_1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; PARTIAL.
 DR PROSITE: PS0186; EGF_2; UNKNOWN.
 DR TRANSFERASE: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Repeat.
 FT DOMAIN 1 541 EXTRACELLULAR (POTENTIAL).
 FT TRAMEM 542 562 POTENTIAL.
 FT DOMAIN 563 584 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 164 300 CYS-RICH.
 FT DOMAIN 301 410 FIBRONECTIN TYPE-III.
 FT DOMAIN 411 527 FIBRONECTIN TYPE-III.
 FT DOMAIN 619 882 PROTEIN KINASE.
 FT SITE 909 984 SAM.
 FT NP_BIND 982 984 PDZ-BINDING MOTIF (POTENTIAL).
 FT BINDING 625 633 ATP (BY SIMILARITY).
 FT ACT_SITE 651 651 ATP (BY SIMILARITY).
 FT MOD_RES 594 594 BY SIMILARITY.
 FT MOD_RES 600 600 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 778 778 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 928 928 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 984 AA: 109519 MW: 109519 MW: EF06C83B63A13A1 CRC64;

Query Match 72.4%; Score 3704; DB 1; Length 984;
 Best Local Similarity 70.2%; Pred. No. 1.3e-221;
 Matches 687; Conservative 120; Mismatches 150; Indels 22; Gaps 3;

QY 7 ETLNDSTATATLAEELGAWVPPSGMEVSGYDENMNTITRYOVGVNESSONMMLTKETIRR 66
 DB 1 ETLNDSTATATLAEELGAWVPPSGMEVSGYDENMNTITRYOVGVNESSONMMLTKETIRR 60
 QY 67 RGAIRIHVEMKESVYDCSSIPVYSGCKEMFNLYYVADDSATKTFPNMKNPWKVD 126
 DB 61 RGAIRITETKRYTDCSSIPVYSGCKEMFNLYYVADDSATKTFPNMKNPWKVD 120
 QY 127 IADSEFSQVLDGGRVKNITEVRSFGVSGFYLAFOYGGCMLIAVRFYRCPR 186
 DB 121 IADSEFSQVLDGGRVKNITEVRSFGVSGFYLAFOYGGCMLIAVRFYRCPR 180
 QY 187 IONGAIFQELLSAEESTSLVAARGSCIANAEVDVPIKLYCNGDGMVLPIGCMKAGF 246
 DB 181 VONFAITPETMTAEESTSLVTARGTCTPNAEVDVPIKLYCNGDGMVLPIGCMKAGF 240
 QY 247 EAVENGTVKCGSGSTFKANQGDGACTHCPINSRTSEGATNCVNGYRRADLDLDP 306
 DB 241 EP-BNNVACACACAGTFFKASQAGLCARCPNRSASAEPLCACRNGYFRADLDPTAA 299
 QY 307 CTTIPSPQAVISVNETSLMLETPPRDSCGREDLVNIIKSCSGSGRACATRCGDNY 366
 DB 300 CTSVPSGPRVVISIVNETSLMLETPPRDSCGREDLVNIIKSCSGSGRACATRCGDNY 359
 QY 367 YABROGLTEPRYISDLAHOYFEIOAVNGVTOQSFQFASVNTTQAAPSAVS 426
 DB 360 FVPROGLTETKRYISDLAHOYFEIOAVNGVTOQSFQFASVNTTQAAPSAVS 419
 QY 427 IMHOVSRIVDSITLSWSPDQPGVITLDELQYERK-----ELSEY 467
 DB 420 IMHOVSRIVDSITLSWSPDQPGVITLDELQYERK-----ELSEY 479
 QY 468 NATATSPNT--VYGLKGAIVYFOVRAVYAGRGSGKATPOTMTEAEVQISQEK 525
 DB 480 NSVVASQNTARLEGLRGAMVYVOVRAVYAGRGSGKATPOTMTEAEVQISQEK 539
 QY 526 PLTIGSSAAGLVLAIVVAVIATVCKNRGERADSEYTKLQHYTGHTPGMKIYIDFT 585
 DB 540 PLTIGSSAAGLVLAIVVAVIATVCKNRGERADSEYTKLQHYTGHTPGMKIYIDFT 599

QY 586 YEDNEAVREPAKEIDISCKYIDQVIGAGEFGVSGHKLTPKREIFVAKTLKSGYTE 645
 DB 600 YEDNEAVREPAKEIDISVFKIEVIGAGEFGVSGHKLTPKREIYVAKTLKSGYTE 659
 QY 646 KORRDFSEASINGOPHPVHLEGVYKSTPVMITTEMNGSLDSFLRQNDGQFTYI 705
 DB 660 KORRDFSEASINGQDHPHITLREGVYKSTPVMITTEMNGSLDSFLRQNDGQFTYI 719
 QY 706 QLVGMILGIAAGKYLADNMYVARDLAARNILVNSLVKVSDFGSLREDTSDPTYT 765
 DB 720 QLVGMILGIAAGKYLAEKMYVARDLAARNILVNSLVKVSDFGSLREDTSDPTYT 779
 QY 766 SAIGKRPIMTAPALIOVRKFTSASDVNSYGTIVMAEVSYSGBRYMDTNDYINAI 825
 DB 780 SLSGKIPKRAVAPALIAVRKFTSASDVNSYGTIVMAEVSYSGBRYMDTNDYINAI 839
 QY 826 DYRLPPEMDCPSALHOLMDCKMDRNRHRCGOIYNTLDKMIKPNNSLKAAAPLSSG 885
 DB 840 DYRLPPEMDCPSALHOLMDCKMDRNRHRCGOIYNTLDKMIKPNNSLKAAAPLSSG 899
 QY 886 LPLDRTIDYTSFNTVDEMLEIKMGQYKESFANAGTSPDVNSQMMEDILRVGYTLA 945
 DB 900 QPLDRTIDYTSFNTVDEMLEIKMGQYKESFANAGTSPDVNSQMMEDILRVGYTLA 959
 QY 946 GHQKILNSIQVRAQOMQ 964
 DB 960 GHQKILNSIQVRAQOMQ 978

RESULT 9
 EPB3_CHICK
 ID EPB3_CHICK STANDARD; PRT: 988 AA.
 AC 007498;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPHRIN TYPE-B RECEPTOR 3 (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK10) (FRAGMENT).
 GN EPHB3 OR CEK10.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=93288394; PubMed=8510926;
 RA Sajjadi F.G., Pasquale E.B.;
 RT "Five novel avian Eph-related tyrosine kinases are differentially expressed."
 RL Oncogene 8:1807-1813(1993).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PRESENT IN 10-DAY EMBRYONIC BRAIN AND BODY TISSUES. PROMINENT EXPRESSION IN KIDNEY. LOWER EXPRESSION IN LUNG, AND BARELY DETECTABLE IN BRAIN, LIVER, HEART, SKELETAL MUSCLE AND THYMUS.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: BEYONDS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.
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[illegible]

SEQUENCE 988 AA; 1095/8 MW; EEAUD39C03FFD5C6 CRC04

Matches 683; Conservative 120; Mismatches 144; Indels 29; Gaps 0.

316 AVISSVNETSLMLEWTPPRDSGGKEDLVNLLCKSCGSGKACIRCGDNVQIAFKVL 312

9/3 10PM RLEQMNQI LEVQV 500

CC EPHKLIN-B1 AND -B2

OncoGene 8:2857-2862(1993).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO EPHRIN-B1 AND -B3.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X75208; CAA53021.1; -
 CC HSSP: P00523; 2PTK.
 CC MIM: 601839; -
 DR InterPro: IPR000719; -
 DR InterPro: IPR001090; -
 DR InterPro: IPR001245; -
 DR InterPro: IPR001426; -
 DR InterPro: IPR001650; -
 DR InterPro: IPR001777; -
 DR Pfam: PF001404; EPH_Lbd; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00014; ENTPEPIT.
 DR PRINTS: PR00109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00119; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR Transfaser: Tyrosine-protein kinase: ATP-binding: Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 33
 FT CHAIN 34 998
 FT DOMAIN 34 598
 FT TRANSMEM 560 580
 FT DOMAIN 581 998
 FT DOMAIN 199 336
 FT DOMAIN 337 448
 FT DOMAIN 449 544
 FT DOMAIN 633 896
 FT DOMAIN 923 998
 FT SITE 998
 FT NP_BIND 639 647
 FT BINDING 665 665
 FT ACT_SITE 758 758
 FT MOD_RES 608 608
 FT MOD_RES 614 614
 FT MOD_RES 792 792
 FT MOD_RES 942 942
 FT CARBOHYD 351 351
 FT CARBOHYD 445 445
 SQ SEQUENCE 998 AA; 110286 MW; 57C82C397CC61103 CRC64;

Query Match 71.0%; Score 3632.5; DB 1; Length 998;
 Best Local Similarity 70.5%; Pred. No. 3.5e-217;
 Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

QY 4 AVEETLMDSTFATLGMVHPSPGMEVSGDEMNMTIRTYOVCNVPESSQNMWLRTKF 63
 DB 37 ALEETLMOTKWTSLATSHRESGHEVSGDEAMNIRTYOVCNVPESSQNMWLRTGF 96
 QY 64 IRRRAHRIHEMKFSPVDCSSIPSPGCKETFNLYYEADEFPSATRTFFNMENPMVK 123
 DB 97 IWRDVORHVVVELKFTVDCNSIPNIPGCKETFNLYYEADEFPSATRTFFNMENPMVK 156

QY 124 VDTIADDESQVLDGRVWKINTFVRSFGPVSRSGFYLAFODYGCSMLAVRVFKC 183
 DB 157 VDTIADDESQVLDGRVWKINTFVRSFGPVSRSGFYLAFODYGCSMLAVRVFKC 212
 QY 184 PRITONGAIFOEFLSCAESTSLVAANGSCIANAEVDVPIKLYCNGDGMVLPIRCKCK 243
 DB 213 ASPTAGFALFPELTIGAEPTSLVIAFGTIPNAVEVSPKLYCNGDGMVPGACCTCA 272
 QY 244 AGEFAVENGTGRCGCESTFKNAGODEACTHCPINSTRITSEGTACVCRNGYRDLPL 303
 DB 273 TGHEPAKESQCRPCPGSKYAKOGEGPCLPCPRMSRTSPASICTCHNNFRADSDSA 332
 QY 304 DMCCTIPAPQAVISSVETSLMEPTPPRSGREDLVNITICKSC--GSGRGACTRC 361
 DB 333 DSACTIVSPRPGVLSNWNETSLLIEMSEPRDLGVRDLLVNICCKKHGAGGASCSRC 392
 QY 362 GDNVYAPRQLGLTEPRYISDLAHTQYTFEIQAVNGCVTQSPSPQFASVNTTNOA 421
 DB 393 DNVFVRPQGLSBRVHTSHLAHTRYTEVQAVNGVSGSKPLPPRYAANVITNOA 452
 QY 422 PSANVIMQSTVSTLSMSQDPNGVILDYELQYERELSEYNATAIKSPNTV-- 479
 DB 453 PSEVPTLRHSSGSSSLTSLSNAPRPERNGVILDYEMKTFEK--SEGIASTVSGMNSVOL 510
 QY 480 TGLKAGAIYFQVRYATVAGYGRYSCKMYFOTME-AEYQTSIDKPLTIGSSAGLVF 538
 DB 511 DGLRPDARTVQVRYATVAGYGRYSCKMYFOTME-AEYQTSIDKPLTIGSSAGLVF 570
 QY 539 LIAVVVIAVCRNGFERADEBYTDLQHYTSGHITPGMKIYIDPFYEDPNEVREFAK 598
 DB 571 VVAVVVIAVCRNGFERADEBYTDLQHYTSGHITPGMKIYIDPFYEDPNEVREFAK 626
 QY 599 EDISCVKIEBOVIGAGEGECGHLKPKGRELFVAIKTLKSYTEKORDELSEASIM 658
 DB 627 EIDVSCVIEEYIGAGEGECGHLKPKGRELFVAIKTLKSYTEKORDELSEASIM 686
 QY 659 GQDFHPVNIHLEGVYTKSTPVMTTEFEMENGLSDFRONDGOFTYQLGMLRGTAAG 718
 DB 687 GQDFHPVNIHLEGVYTKSTPVMTTEFEMENGLSDFRONDGOFTYQLGMLRGTAAG 746
 QY 719 KYLDAMNVHDLAARNLVNSNLVCKVSPDGLSRPLEDDTSPTYSALGKFRPRTWA 778
 DB 747 KYLDAMNVHDLAARNLVNSNLVCKVSPDGLSRPLEDDTSPTYSALGKFRPRTWA 806
 QY 779 PEATQYKFTSASDVMSYGIYMEVMSYGERPMDNODVINAIEDVRLPPMDCPSA 838
 DB 807 PEATQYKFTSASDVMSYGIYMEVMSYGERPMDNODVINAIEDVRLPPMDCPSA 866
 QY 839 LHQMLDCKORNRHRRKFGQIYNTLDKMRNPNLSKAMAPLSSGINPLDLRTTIDYTS 898
 DB 867 LHQMLDCKORNRHRRKFGQIYNTLDKMRNPNLSKAMAPLSSGINPLDLRTTIDYTS 926
 QY 899 FNTVDENVLEAIKMGQYSEFANAGFTSPDVVSOMMEDILRVYTLAGOKTLNSIQW 958
 DB 927 FNTVDENVLEAIKMGQYSEFANAGFTSPDVVSOMMEDILRVYTLAGOKTLNSIQW 986
 QY 959 RAQMNQIQSYEV 970
 DB 987 RLQMNQTLPIVOV 998

RESULT 11
 EPHRIN_MOUSE
 ID EPHRIN_MOUSE STANDARD; PRT; 993 AA.
 AC P54754; 062214; Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR MOK-5) (DEVELOPMENTAL KINASE 5) (SEK-4).
 GN EPHRIN OR ETK2 OR MOK5 OR SEK4.
 OS Mus musculus (Mouse).

QY 716 AGMKYLADNNYVHRDLAARNLIVNSLVCKVSDFLSRLFEDDTSPTYTALSGKPEIR 775
 Db 739 AGMKYLSENNYVHRDLAARNLIVNSLVCKVSDFLSRLFEDDTSPTYTALSGKPEIR 798
 QY 776 WTAPAEIORYKFTSADSWYGVIVWMEVMSYGERPYNMTNODYNAIEODYRLPPEMDC 835
 Db 799 WTAPAEIARYKFTSADSWYGVIVWMEVMSYGERPYNMTNODYNAIEODYRLPPEMDC 858
 QY 836 PEAHLQMLDCWQKDRNHRPKFGQIVNTLDKMRNPSLAKMAPLSGGINPLDRTIPD 895
 Db 839 PTAHLQMLDCWQKDRNHRPKFGQIVNTLDKMRNPSLAKMAPLSGGINPLDRTIPD 918
 QY 896 YTSFTVDEMTEATKMGYKSPFANAGTSPDYVSQMMEDILNVTGLAGHOKKIINSTI 955
 Db 919 YTSFTVDEMTEATKMGYKSPFANAGTSPDYVSQMMEDILNVTGLAGHOKKIINSTI 978
 QY 956 QVMAQNMNQISVEY 970
 Db 979 QDMRLQNMNQISVEY 993

RESULT 12

EPBB_XENLA STANDARD; PRT; 902 AA.

AC Q91736;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE EPHRIN TYPE-B RECEPTOR 1B (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE

GN XELK).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI_TaxID=8335;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96068901; Pubmed=7478602;

RT Scales J.B., Manning R.S., Renaud C.S., Shea L.J., Sargent T.D.;

RT "Novel members of the eph receptor tyrosine kinase subfamily expressed

RL Oncogene 11:1745-1752(1995)."

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY (BY

CC SIMILARITY).

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN

CC TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN THE BRAIN AND

CC SPINAL CORD AND IN THE FIRST AND FOURTH VISCERAL ARCHES. MOST

CC ABUNDANT IN ADULT BRAIN, WITH LOWER LEVELS IN EYE, HEART, OVARY,

CC OVIDUCT, LUNG AND PHARYNX.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

CC -----

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CC -----

CC EMBL: L43621; AAA93527.1; -

DR HSSP: P00523; 2PTRK.

DR InterPro: IPR000719; -

DR InterPro: IPR001090; -

DR InterPro: IPR001245; -

DR InterPro: IPR001426; -

DR InterPro: IPR001660; -

DR InterPro: IPR001777; -

DR Pfam: PF01404; Eph_1bd; 1.
 DR Pfam: PF00356; SAM; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN; 1.
 DR Transferase: Tyrosine-protein kinase: ATP-binding; phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Repeat.
 FT NON_TER 1 1
 FT DOMAIN <1 459
 FT TRANSMEM 460 480
 FT DOMAIN 481 502
 FT DOMAIN 502 527
 FT DOMAIN 528 543
 FT DOMAIN 544 569
 FT ACT_SITE 662 662
 FT MOD_RES 512 512
 FT MOD_RES 518 518
 FT MOD_RES 696 696
 FT MOD_RES 846 846
 FT CARBOHYD 252 252
 FT CARBOHYD 344 344
 FT CARBOHYD 398 398
 SQ SEQUENCE 902 AA; 100850 MM; CCB9ABF7D39273CA CRC64;

Query Match 70.2%; Score 3593.5; DB 1; Length 902;
 Best Local Similarity 73.1%; Pred. No. 7.8e-215;
 Matches 657; Conservative 125; Mismatches 110; Indels 7; Gaps 4;

QY 70 HRIHEMKFSYRDCSSIPVSCKETPNLYYRAD--FSSATTEFPNMMENPVAVDTI 127
 Db 1 HRVYEMKFTYRDCSSLPNVSCKETPNLYYRAD--FSSATTEFPNMMENPVAVDTI 58
 QY 128 AADSFQVNDLGRVNMINEVRSFGVSRSGEFLAQDYGCGMSLAVAVFPRKCPRII 187
 Db 59 AADSFQVNDLGRVNMINEVRSFGVSRSGEFLAQDYGCGMSLAVAVFPRKCPRII 118
 QY 188 ONGALPQETSGAESTSLVARGSCINAAEVDVPIKLYNGDGEWLVPGRCKAGFE 247
 Db 119 ONFAVPEETMGAEESTSLVARGSCINAAEVDVPIKLYNGDGEWLVPGRCKAGFE 178
 QY 248 AVENGVCRCGPGSTFRKANGDEACTHCPINSRTSGATNGCVCRNGYVRADIDPDMC 307
 Db 179 P-ENHVVCKACPAKMPFRANGCMGACQCPANRSSTSEASICICRNGYVRADIDPDMC 237
 QY 308 TTTSAAQAVISSVNESTSLMEWTPPRDSGREDLVYNIICKSGSGRACATRCGDNVOY 367
 Db 238 TTSVSGRNVISVNESTSLMEWTPPRDSGREDLVYNIICKSGSGRACATRCGDNVOY 297
 QY 368 APRQLGTEPRIRYISDLAHTOYTFELQVNGVTDGSPSPQASVNTITNOAAPSVAI 427
 Db 298 VPRQLGTEPRIRYISDLAHTOYTFELQVNGVTDGSPSPQASVNTITNOAAPSVAI 357
 QY 428 MHOVSRTVDSITLSWSPQDPNGVILDEYQYKEKLSSEYNATKSPNT--VTGLKAG 485
 Db 358 MHOVKATKMSITLSWSPQDPNGVILDEYQYKEKLSSEYNATKSPNT--VTGLKAG 417
 QY 486 AIYVFOVRAATVAGYRGSKMYEOTMTAEAYOTSLQELPLITSSAAGVFLAAVVI 545
 Db 418 VYVVOVRAATVAGYRGSKMYEOTMTAEAYOTSLQELPLITSSAAGVFLAAVVI 477
 QY 546 AIVCNRRGERADSEYTDLQHYTSGHITPGMKIYIDPTTYPDPEAVAREFAKEIDISCV 605

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DB 478 SLVSCRRTYSKEAVYSDKLQHYSTGRSPGMKIYIDPTEYEDNEAVREFAKEIDVSVF 537
OY 606 KIEOYIGAGEGECVSSGLKLPGRREIFVALTKTSQTYEORORDPSEASIMGOFDPHN 665
DB 538 KIEEYIGAGEGECVSSGLKLPGRREIFVALTKTSQTYEORORDPSEASIMGOFDPHN 597
OY 666 VTHIEGVYTKSTPVMIIIEFEMENGSLDFLRONDQOFTVIOVLGRLGIAAGMYLADMN 725
DB 598 IIRLEGVYTKSPVMIIIEFEMENGSLDFLRONDQOFTVIOVLGRLGIAAGMYLADMN 657
OY 726 VYHRDLAARNILVNSLVCKVSDGSLDFLEDDTSPTTYTALGSKFPIRMTAEALQYR 785
DB 658 YVHRDLAARNILVNSLVCKVSDGSLDFLEDDTSPTTYTALGSKFPIRMTAEALQYR 717
OY 786 KFTSASDVAWSYGVIMWEMVSYGERPYMTNODVINALTEODYRLPPMDCCSALHQLMLD 845
DB 718 KFTSASDVAWSYGVIMWEMVSYGERPYMTNODVINALTEODYRLPPMDCCSALHQLMLD 777
OY 846 CMQKDRNHRPKRGQIVNTLDMKIRNPNSIKAMAPLSSGILPLDRTIPDYTSFNTVDEW 905
DB 778 CMQKDRNHRPKRGQIVNTLDMKIRNPNSIKAMAPLSSGILPLDRTIPDYTSFNTVDEW 837
OY 906 LEAIKMGQYKESFANAGTSPFVVSOMMEDILRYGVTLGAGHOKIINSIOYMAQNMQ 964
DB 838 LSAIKMGQYKESFANAGTSPFVVSOMMEDILRYGVTLGAGHOKIINSIOYMAQNMQ 896
OY 964 LEAIKMGQYKESFANAGTSPFVVSOMMEDILRYGVTLGAGHOKIINSIOYMAQNMQ 964
DB 838 LSAIKMGQYKESFANAGTSPFVVSOMMEDILRYGVTLGAGHOKIINSIOYMAQNMQ 896

RESULT 13
EPB3_XENLA STANDARD: PRT: 974 AA.
ID EPB3_XENLA
AC 091735;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
KINASE RECEPTOR TKC).
OS TKC.
GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9608901; PubMed=7478602;
RA Scales J.B., Winnick R.S., Renaud C.S., Shea L.J., Sargent T.D.;
RT "Novel members of the eph receptor tyrosine kinase subfamily expressed
during xenopus development.";
RT Oncogene 11:1745-1752(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY (BY
SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN PRE-SOMITIC
MESODERM, CAUDAL SOMITES, MIDBRAIN, AND CEMENT GLAND. MOST
ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER LEVELS
IN TESTES, KIDNEY, OVIDUCT AND PHARYNX.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
RECEPTOR SUBFAMILY.
CC -----
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CC or send an email to license@isb.ch).
CC -----
DB EMBL; LA3620; AAA93526.1; -

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DR HSP: P29323; 1BAF.
DR InterPro: IPR000719; -
DR InterPro: IPR001090; -
DR InterPro: IPR001245; -
DR InterPro: IPR001426; -
DR InterPro: IPR001660; -
DR InterPro: IPR001777; -
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; PKinase; 1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF01404; Eph_Lbd; 1.
DR PRINTS: PRO0014; ENTYPEIIT.
DR PRINTS: PRO00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 15
FT CHAIN 1 974
FT DOMAIN 17 534
FT TRANSMEM 535 553
FT DOMAIN 556 974
FT DOMAIN 178 315
FT DOMAIN 316 423
FT DOMAIN 424 520
FT DOMAIN 609 872
FT DOMAIN 899 974
FT SITE 972 974
FT NP_BIND 615 623
FT DISULFID 60 95
FT BINDING 641 641
FT ACT_SITE 734 734
FT MOD_RES 584 584
FT MOD_RES 590 590
FT MOD_RES 768 768
FT MOD_RES 918 918
FT CARBOHYD 330 330
FT CARBOHYD 420 420
FT SEQUENCE 974 AA; 108263 MW; F881412E8628533 CRC64;

Query Match 67.7%; Score 3465.5; DB 1; Length 974;
Best Local Similarity 66.2%; Pred. No. 7.2e-207;
Matches 645; Conservative 142; Mismatches 172; Indels 15; Gaps 6;

OY 2 LAAV---EETLMDSTATAELGAMVHPSPGMEVSGYDENMNTIRTYQVNFESSQNMV 58
DB 11 LSAVGLLEETLMDIKWTTSSELAWAVPDGWEVSGYDEASNPRTIYQVNVDRSNNMV 70
OY 59 LTRKFRRRGARHRIHVENKFSVRDSSIPVSGCKETFNLYYEADPSATKTFPMWME 118
DB 71 LRTQITIPRODQVRYVELKFTVRODONSPLNRGSCKEFNFFYESDSDSADSPRME 130
OY 119 NPWVAVDTIADDESQVDLGRWKITEVRSRPSRSEFYAFDPDYGCSMLIAYRV 178
DB 131 NPYIKVDITADPESFSRDSG---RVNTKIRSFEPISRAEFTYAFDGLGACVLSIVRV 186
OY 179 FYRKPRPIIONAIFQETLSGAEASTLVAAGSCIANAEVDPVPIKLYCNGDGEMLVPIG 238
DB 187 FKKCPRTTAGASAPPEITLGAEPISLVIAAGTCVPNALLEVSVPLKLYCNGDGMVAVPG 246
OY 239 RCMKAGFEAVENGTVCRGCPSTGRKANQGDACHTHCINSRTISEGATNCVGRNGYRA 298
DB 247 ACTCAAGFEPAKDKTYCCACKRGTYKSKQGRGSCMPCANRAISAAITCSQNGYTRA 306
OY 299 DDDPDMPTTIPSAQVAVSSVNTSLMLEWTPRODGGREDVLYNICKSCSGSRGAC 358
DB 307 DEESATFCTSPASAPROVISVNETSVYLENAEPGHGAGDVLVYNIKKC--LERLC 364
OY 359 TRCGDNVQYAPRQGLITEPRIVISDLAHTQYTFEIQAVNGVTDGSPSPQASVNIITN 418

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Db 365 SHCDDNVCWPPQOLGTVTQTLVSVSHQAHTRKSFELQAVNGSGKSPHPIPVYFTVNTTN 424
Oy 419 QAAPSASVIMHOVSRVITLWSQDPQNGVILDELYEYER-ELSEYVATAIKSTPN 477
Db 423 QAAPSASVIMHOVSRVITLWSQDPQNGVILDELYEYER-ELSEYVATAIKSTPN 484
Oy 478 TVTGAKAIVYFOVRATVAGYGRSGKMTFQWTAEVQTSIOEKLPLIISSAGLV 537
Db 485 RHEGHTPPTVYVVOVRATVAGYGRSGKMTFQWTAEVQTSIOEKLPLIISSAGLV 544
Oy 538 FLIAVVAIAYC-NRGERADSEYTDKLOHVTGSHITPGKTIIDPTPYEDPNEANREF 596
Db 545 FLIAVVAIAYC-NRGERADSEYTDKLOHVTGSHITPGKTIIDPTPYEDPNEANREF 600
Oy 557 AKEDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLEAS 656
Db 601 AKEDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLEAS 660
Oy 657 IMGOFDHPNVIHLGGVYKSPVMIITEFPMNGSLDFLRQNGOFTVIOLVGMLGRTAA 716
Db 661 IMGOFDHPNVIHLGGVYKSPVMIITEFPMNGSLDFLRQNGOFTVIOLVGMLGRTAA 720
Oy 717 GMKYLADNIVYHDLAARNILVNSLVCKVSDFGLSFLEDDTSDPTYSALGKPIRW 776
Db 721 GMKYLADNIVYHDLAARNILVNSLVCKVSDFGLSFLEDDTSDPTYSALGKPIRW 780
Oy 777 TAPALIOYKRTSADVWSYGIYMEVWSYGERPYMDTNOVYIMAEODYRLPPMDCP 836
Db 781 TAPALIOYKRTSADVWSYGIYMEVWSYGERPYMDTNOVYIMAEODYRLPPMDCP 840
Oy 837 SALHQLMDCMQKDRNRPFGQIVNTLDKIRNPNSLKMALSSGINSPLDRTITPOY 886
Db 841 SALHQLMDCMQKDRNRPFGQIVNTLDKIRNPNSLKMALSSGINSPLDRTITPOY 900
Oy 897 TSPTVTEMLAIKMGQYKESFANAGTSPDVVSQMMEDILRVGYTLGHQKIKINSIQ 956
Db 901 TSPTVTEMLAIKMGQYKESFANAGTSPDVVSQMMEDILRVGYTLGHQKIKINSIQ 960
Oy 957 VMRAQNMQIOSEVY 970
Db 961 VMRAQNMQIOSEVY 974

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CC CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
CC CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC CC -1- PROTEIN TYROSINE PHOSPHATE.
CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THYMUS AND DETECTABLE IN
CC CC BRAIN, RETINA, KIDNEY, LUNG, AND HEART. NOT DETECTED IN SKELETAL
CC CC MUSCLE AND LIVER.
CC CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC CC RECEPTOR SUBFAMILY.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: U23783; AAB41054.1; -.
CC CC HSSP: P00523; 2PTK.
CC CC InterPro: IPR000561; -.
CC CC InterPro: IPR000719; -.
CC CC InterPro: IPR001090; -.
CC CC InterPro: IPR001245; -.
CC CC InterPro: IPR001426; -.
CC CC InterPro: IPR001660; -.
CC CC InterPro: IPR001777; -.
CC CC Pfam: PF01404; EPH_Lbd; 1.
CC CC Pfam: PF00536; SAM; 1.
CC CC Pfam: PF00041; fn3; 2.
CC CC Pfam: PF00069; kinase; 1.
CC CC PRINTS: PR00014; FNTYPEPIL.
CC CC PRINTS: PR00109; TYRKINASE.
CC CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC CC PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
CC CC PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
CC CC PROSITE: PS01186; EGF_2; UNKNOWN_1.
CC CC KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
CC CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
CC CC FT SIGNAL 1 29
CC CC FT CHAIN 30 1002
CC CC FT DOMAIN 30 564
CC CC FT TRANSMEM 565 585
CC CC FT DOMAIN 586 1002
CC CC FT DOMAIN 195 338
CC CC FT DOMAIN 339 449
CC CC FT DOMAIN 450 547
CC CC FT DOMAIN 637 900
CC CC FT DOMAIN 862 865
CC CC FT DOMAIN 927 1002
CC CC FT SITE 1000 1002
CC CC FT NP_BIND 643 651
CC CC FT BINDING 669 669
CC CC FT ACT_SITE 762 762
CC CC FT MOD_RES 612 612
CC CC FT MOD_RES 618 618
CC CC FT MOD_RES 796 796
CC CC FT MOD_RES 946 946
CC CC FT CARBOHYD 446 446
CC CC SQ SEQUENCE 1002 AA; 111947 MW; 6D9635B500DB0DA CRC64;

```

Query Match 65.3%; Score 3341.5; DB 1; Length 1002;
 Best Local Similarity 62.9%; Pred. No. 3.5e-199;
 Matches 617; Conservative 152; Mismatches 197; Indels 15; Gaps 7;

Oy 1 LLAVEETLMDSTTATAEIGMWHPPSGEVEYSGYDENNMHTITTYOVCAVFPSSQNMHLR 60
 Db 26 LVTSLEETLMDTGTGEMSEIGMTSHPPDGMVEYVVRDCKRQIRITGVCAVMDPQGNMHLR 85

FT MOD_RES 595 595 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 601 601 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 778 778 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 928 928 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED GLCNAC. . . (POTENTIAL).
 FT CARBOHYD 407 407 N-LINKED GLCNAC. . . (POTENTIAL).
 SO SEQUENCE 986 AA: 109840 MW: C34F4078B3F023F-CRC64;

Query Match 60.0%; Score 3070; DB 1; length 986;
 Best Local Similarity 60.1%; Pred. No. 2,1e-182;
 Matches 582; Conservative 147; Mismatches 218; Indels 22; Gaps 11;

QY 4 AVEETLMSTFTALGMMVHP-PSGEEVSGYDENMTFTTYOVCNVESSQNNMLRTK 62
 DB 28 ASEVTLDSRSVQELGVIASLEGMEVEIMDEKNTPIRTYQVCNVESSQNNMLRTD 87
 QY 63 FIRRGARIRIHMEKFSYRDCSSIPVSGCKETFNLYYEADFDSDATKTPNNMKNPV 122
 DB 88 WIPRSGAQRVVEIKFTLRDCNSLPVGWGTCKETFNLYYESNNDKERFT---RETQYV 143
 QY 123 KVDITADESTQVDLGRVKKINTEVRSFGVSRSGFYLAFODYGCMSLIAVRYFRK 182
 DB 144 KIDITADESTFOVDIGDRIMKLTENVVDVPLSKGFIYAFODVGACIALVSVRYFRK 203
 QY 183 CPRIONGAIFQETLGAESTSLAARGSCIANAEVDVPIKLYCNGDGEWLPVIGRCMC 242
 DB 204 CPLVYRNLAQFPDITTSDSISLVEVSGSCVDNSEKDVV-KMYCGADGEMLVPIGNCIC 262
 QY 243 KAGEVAENGTVCRGCPGTFKANOGEACTHCPINSRTSEGTNCVCNRYRADLDP 302
 DB 263 NAGFEHNCG--CGACKVGYKALSTDAACKCPHYALREGSTCTCDRGIFRADTDP 320
 QY 303 LDNCTTIPSPAPQVIVSSVNETSLMLEWTPRDSGREDLVYNIICKSCSGRGACTRCG 362
 DB 321 ASMCPTRPSPAPQVILISVNETSVNLEMSPPNGSGRPDVSYNLVCKRCGSDLTRCRPG 380
 QY 363 DNVQAPROGLTEPRYISDLAHTQTEIOAVNGVTDOSSPSPQFASVNTTNOAP 422
 DB 381 SGVHSPQONGKLTKTSTIDLOAHNTYFEVWSINGVSKONPQODAVSVTITNOAP 440
 QY 423 SAVSIMHOVSTVDSITLSMSOPDPNGVILDELOYEKELESEYNATAIKSPNT--VT 480
 DB 441 STVYQIQPKDITRHSVSLTWPEPRPGVILEYEVKYEKQNERTRYRIYKITSRSADIK 500
 QY 481 GLKAGAIYVQVARTVAGYRGSKMYFQTMTEAEYQTSIQEKLPIIGSSAAGLVFLI 540
 DB 501 GLNPLTAVYHVHARTAGAGGERSGPEFTTNTVPSPMIG-EGASPTVLLVSAAGSIVLY 559
 QY 541 AVVYIAIVCNRR--GFERADSEYTDKLOHTSGHITPGMKIYIDPTEYEDPNVAREFAK 598
 DB 560 VILIAAFVISRRRSKYSKAKQEADE-----KHLNQGAKTYVDPPTYEDPNQAVREFAK 613
 QY 599 EIDISCKIIOVYIGAGBEGVSGHLKLPGRKEIFVAIKLKSQYTEKORDFLSEASIM 658
 DB 614 EIDASCICKIEKIVGEGFEVSGRLKVPGRKEIYVAIKLKGAYTDKQRPDLSEASIM 673
 QY 659 GQEDHPNVILHEGVYTKSPVMIITEPEMNGSIDSLRONDQGFYIOLVGLRGIAAG 718
 DB 674 GQEDHPNVILHEGVYTKSPVMIITEPEMNGSIDSLRONDQGFYIOLVGLRGISGM 733
 QY 719 KYIADANVYHRIADANILVNSNLVCKVSDFGLSRLEDDTSDPTYSALGKFPIMRTA 778
 DB 734 KYLSDSYVYHRIADANILVNSNLVCKVSDFGMSVLEDD-PEAAVYTR-GGKIPIMRTA 791
 QY 779 PEAIQYRKFTSADVSYGVIMVEVWSYGERPYWMTNODVINAIBODYRLPPMDCPSA 838
 DB 792 PEAIQYRKFTSADVSYGVIMVEVWSYGERPYWMTNODVINAIBODYRLPPMDCPIA 851
 QY 839 LKQJLMDCKQKDRNHRPKFGQIVNTLDKMIIRNPNSIKAWA-PLSSGINPLIDRTIPDYT 897
 DB 852 LKQJLMDCKQKDRNHRPKFGQIVNTLDKMIIRNPNSIKAWA-PLSSGINPLIDRTIPDYT 911

QY 898 SFNTVDEMLFAIKMGQYKESFANAGTSPVVSQMMEDILRYGVTLACHQKKILNSIQV 957
 DB 912 QVASVLDMLQAIKMERKYNFTAGYTSLEAVYHVNODDLTRIGISSPSHONKILSSVOG 971
 QY 958 MRAQMNQIQ 966
 DB 972 MRTQMQIQ 980

Search completed: July 24, 2001, 16:32:38
 Job time: 204 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:28:49 ; Search time 34.42 seconds

(without alignments)
3728.526 Million cell updates/sec

Title: US-09-378-759-11

Sequence: 1 LLAVERETLMDSTTAELG.....LINSIQVRAQNMQISVEV 970

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_16:*
1: SP_Archaea:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_MHC:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Unclassified:*
13: SP_Vertebrate:*
14: SP_Virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5082	99.3	994	11	O9QVY4
2	3734.5	73.0	815	13	O57458
3	3429	67.0	938	11	O60669
4	2917.5	57.0	983	4	O9H2V4
5	2818.5	55.1	552	4	O9H4H4
6	2814.5	55.0	621	4	O9H4H3
7	2723.5	53.2	987	13	O73875
8	2691	52.6	1005	4	O9NUA9
9	2682.5	52.4	880	13	O73879
10	2674	52.3	976	13	O73878
11	2332	45.6	853	4	O9P269
12	2300.5	45.0	977	13	O9PWR5
13	2028	39.6	1080	5	O9Y1J0
14	2024	39.6	1047	5	O9Y1J0
15	2017	39.4	1035	5	O9XZL6
16	2017	39.4	1096	5	O9Y4E5
17	1923.5	37.6	1019	5	O9G435
18	1877.5	36.7	977	11	O9ESJ2
19	1638	32.0	353	13	O9PVV2

20	1623	31.7	353	13	O9U8W2	O9U8W2 eptatretus
21	1617.5	31.6	666	13	O73876	O73876 brachydantio
22	1572.5	30.7	490	13	O73877	O73877 brachydantio
23	1464	28.6	539	4	O9H2V3	O9H2V3 homo sapien
24	1422	27.8	1122	5	O61460	O61460 caenorhabd1
25	1326.5	25.9	893	5	O9Y1Y3	O9Y1Y3 ephydactia f
26	1311	25.6	353	13	O9U8V9	O9U8V9 eptatretus
27	1310.5	25.6	349	13	O9U8W1	O9U8W1 eptatretus
28	1299.5	25.4	348	13	O9U8W0	O9U8W0 eptatretus
29	1292.5	25.3	350	13	O9PVV1	O9PVV1 lampetra re
30	1253	24.5	323	13	O91734	O91734 xenopus lae
31	1252.5	24.5	919	5	O21477	O21477 caenorhabd1
32	1143	22.3	342	5	O9U8V8	O9U8V8 branchiosto
33	1137	22.2	277	4	O9H124	O9H124 homo sapien
34	782.5	15.3	334	4	O9UFC3	O9UFC3 homo sapien
35	771.5	15.1	502	13	O9DDK6	O9DDK6 xenopus lae
36	630	12.3	1362	13	O9DDK6	O9DDK6 salmo salar
37	607	11.9	812	14	O85466	O85466 avian sarco
38	606	11.8	1504	5	O9YV86	O9YV86 drosophila
39	603.5	11.7	348	4	O9UMJ5	O9UMJ5 homo sapien
40	600.5	11.7	383	4	O9NUA4	O9NUA4 homo sapien
41	600.5	11.7	505	4	O9H5Y5	O9H5Y5 homo sapien
42	600.5	11.7	488	13	O13064	O13064 xenopus lae
43	599	11.7	1371	11	O9UWV4	O9UWV4 rattus sp.
44	598.5	11.6	496	4	O9WYV8	O9WYV8 homo sapien
45	594	11.6	4			

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	994 AA.
O9QVY4			
AC	O9QVY4:		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	NEURAL KINASE, NUK-BPH/ELK/ECK FAMILY RECEPTOR-LIKE TYROSINE KINASE.		
OC	Mus sp.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OK	NCBI_Taxid=10095;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94181250; PubMed=8134103;		
RA	Henkemeyer M., Marengere L.E., McGlade J., Olivier J.P., Conlon R.A.,		
RA	Holmwyd D.P., Letwin K., Pawson T.;		
RT	"Immunolocalization of the Nuk receptor tyrosine kinase suggests roles		
RT	in segmental patterning of the brain and axonogenesis.";		
RL	Oncogene 9:1001-1014(1994).		
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN		
CC	TYROSINE PHOSPHATE (BY SIMILARITY)		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN		
CC	RECEPTOR SUBFAMILY.		
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.		
CC	HSSP: P06339; 3ICK.		
CC	InterPro: IPR000561; -		
CC	InterPro: IPR000719; -		
CC	InterPro: IPR001090; -		
CC	InterPro: IPR001245; -		
CC	InterPro: IPR001426; -		
CC	InterPro: IPR001660; -		
CC	InterPro: IPR001777; -		
CC	Pfam: PF00041; fn3; 2.		
CC	Pfam: PF00069; pkinase; 1.		
CC	Pfam: PF00536; SAM; 1.		
CC	Pfam: PF01404; EPH_1bd; 1.		
CC	PRINTS: PR00014; ENTYPETIT.		
CC	PRINTS: PR00109; TYRKINASE.		
CC	PROSITE: PS01186; EGF_2; UNKNOWN_1.		
CC	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.		

DR PROSITE; PS50011: PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00109: PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790: RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791: RECEPTOR_TYR_KIN_V_2; 1.
 DR SMART; SM00454; SAM; 1.
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;
 KW Transferase; Transmembrane; Tyrosine-protein kinase.
 SEQUENCE 994 AA; 110759 MW; BC6B9B12A070394C CRC64;

Query Match 99.3%; Score 5082; DB 11; Length 994;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

1 LIAAEEETLMSTTATTAELGMMVHPSPGMEEYSGYDENMNTIRTYQVNCVFESSQNMMLR 60
 23 LIAAEEETLMSTTATTAELGMMVHPSPGMEEYSGYDENMNTIRTYQVNCVFESSQNMMLR 82
 61 TFFIRRGARHRIHVEKESVSDCSSIPSPGSKETFMUYEADPDSATRTFPMMEHP 120
 83 TFFIRRGARHRIHVEKESVSDCSSIPSPGSKETFMUYEADPDSATRTFPMMEHP 142
 121 WKVVDTIADSFQVVDLGGRYMKINTFVRSRGPVSRSGFYLAFOYGGCMLIAVRYFY 180
 143 WKVVDTIADSFQVVDLGGRYMKINTFVRSRGPVSRSGFYLAFOYGGCMLIAVRYFY 202
 181 RKPRIIONGAIFQETLSGAEISTLVANGSCIANAEVDVPIKLYCNGDEMLVPIGRC 240
 203 RKPRIIONGAIFQETLSGAEISTLVANGSCIANAEVDVPIKLYCNGDEMLVPIGRC 262
 241 MCKAGEAVENGTVCGCGSGTFKANKOGDEACTHCPINSRTSECATNVCNGYRADL 300
 263 MCKAGEAVENGTVCGCGSGTFKANKOGDEACTHCPINSRTSECATNVCNGYRADL 322
 301 DPLDMCTTIPSPAPAVISVNETSLMLEMTPPRSGREDLVYNIICKSCSGRGACTR 360
 323 DPLDMCTTIPSPAPAVISVNETSLMLEMTPPRSGREDLVYNIICKSCSGRGACTR 382
 361 CGDNVQAPRQGLTEPRITISDLAHQYTFEIQAVNGVTQSPSPFASVNTTNOA 420
 383 CGDNVQAPRQGLTEPRITISDLAHQYTFEIQAVNGVTQSPSPFASVNTTNOA 442
 421 APASVSIIMHGVSTVDSTILTSMSOPDOPNGVILDEYQYEEKLSYNTATIKSPNTYT 480
 443 APASVSIIMHGVSTVDSTILTSMSOPDOPNGVILDEYQYEEKLSYNTATIKSPNTYT 502
 481 --GLKAGAIYVQVRAATVAGYGRYSKMYFQMTAEAYQTSIQEKLPLIIGSSAAGLVF 538
 503 VQGLKAGAIYVQVRAATVAGYGRYSKMYFQMTAEAYQTSIQEKLPLIIGSSAAGLVF 562
 539 LIAAVVTAIYCNRRGFRADSETTDKIQHTSGHITPQMKIYIDPTEYEDPNAVEEPAK 598
 563 LIAAVVTAIYCNRRGFRADSETTDKIQHTSGHITPQMKIYIDPTEYEDPNAVEEPAK 622
 599 EIDISCVKTIQVIGAGFEYGCSTGLPKGRLEIFVAIKTLKSGYTEKORDELSEASIM 658
 623 EIDISCVKTIQVIGAGFEYGCSTGLPKGRLEIFVAIKTLKSGYTEKORDELSEASIM 682
 659 GQDFHPNVILHEGVYKSTPYMTTEFEWNGSLDSELRONDQGFYVQLVGMRLGIAAGM 718
 683 GQDFHPNVILHEGVYKSTPYMTTEFEWNGSLDSELRONDQGFYVQLVGMRLGIAAGM 742
 719 KYLADNMVYHHDLAARNITVNSNLVCKVSDFGLSRFLLEDITSDPTTYSALGKFIPIWTA 778
 743 KYLADNMVYHHDLAARNITVNSNLVCKVSDFGLSRFLLEDITSDPTTYSALGKFIPIWTA 802
 779 PEALQYRKETASDVWSYGIYVMEVMSYGERPYWMTNODVINAIEDYRLPPMDCPSA 838
 803 PEALQYRKETASDVWSYGIYVMEVMSYGERPYWMTNODVINAIEDYRLPPMDCPSA 862
 839 LHQMLDQWQDRNRHRRFQGIYVNTLDKMTFNPSLTKAMAPLSSGILNPLIDRTIPIYTS 898
 863 LHQMLDQWQDRNRHRRFQGIYVNTLDKMTFNPSLTKAMAPLSSGILNPLIDRTIPIYTS 922

QY 899 ENTVDMELEAIKMGQYKESFANAGFTSPDYVSOMMEDILRYGVTLAGHOKIILNSIQVM 958
 DB 923 ENTVDMELEAIKMGQYKESFANAGFTSPDYVSOMMEDILRYGVTLAGHOKIILNSIQVM 982
 QY 959 RAOMNOIOSVEV 970
 DB 983 RAOMNOIOSVEV 994

RESULT 2
 ID 057458 PRELIMINARY; PRT: 815 AA.
 AC 057458;
 DT 01-JUN-1998 (TREMEL; 06, Created)
 DT 01-JUN-1998 (TREMEL; 06, Last sequence update)
 DT 01-MAR-2001 (TREMEL; 16, Last annotation update)
 DE EPHB2-TYROSINE KINASE RECEPTOR (FRAGMENT).
 GN XEPHB2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanaka M., Wang D.Y., Kamo T., Igarashi H., Wang Y., Xiang Y.Y.,
 RA Tanaka F., Naitoh Y., Sugimura H.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
 CC -1- TYROSINE PHOSPHATE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 DR EMBL; AF026039; AB94603.1; -.
 DR HSSP; P29323; 1B4F.
 DR InterPro; IPR000561; -.
 DR InterPro; IPR000719; -.
 DR InterPro; IPR001245; -.
 DR InterPro; IPR001426; -.
 DR InterPro; IPR001660; -.
 DR InterPro; IPR001777; -.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPR11.
 DR PRINTS; PR00109; TYRKINASE.
 DR PROSITE; PS01186; EGT_2; UNKNOWN_1.
 DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR SMART; SM00454; SAM; 1.
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;
 KW Transferase; Transmembrane; Tyrosine-protein kinase.
 FT NON_TER 1
 FT 1
 SEQUENCE 815 AA; 90848 MW; D36D77C498097BFE CRC64;

Query Match 73.0%; Score 3734.5; DB 13; Length 815;
 Best Local Similarity 86.9%; Pred. No. 2,4e-275;
 Matches 708; Conservative 49; Mismatches 55; Indels 3; Gaps 2;

QY 159 GFYLAFOYGGCMLIAVAVFYRKCPRIIONGAIFQETLSGAEISTLVANGSCIANAE 218
 DB 1 GFYLAFOYGGCMLIAVAVFYRKCPRIIONGAIFQETLSGAEISTLVANGSCIANAE 60
 QY 219 VDVPIKLYCNGDEMLVPIGRCMCKAGEAVENGTVCGSGTFKANKOGDEACTHCPIN 278
 DB 61 VDVPIKLYCNGDEMLVPIGRCMCKAGEAVENGTVCGSGTFKANKOGDEACTHCPIN 120

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OY 279 SRTTSGATNCVCRNGYRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGG 338
DB 121 SRTTSGATNCVCRNGYRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGG 180
OY 339 REDLVNIIICKSGSGRGACTRCGDNVOYAPQOLGTEPRYIYISDLAHOTYTFEIQAVN 398
DB 181 REDLVNIIICKSGSGRGACTRCGDNVOYAPQOLGTEPRYIYISDLAHOTYTFEIQAVN 240
OY 399 GVTDSQFSPFASVNIITNQAPSAVSIMHOVSRVDSITLSMSPQPOPNVILLIDELQ 458
DB 241 GVTDSQFSPFASVNIITNQAPSAVSIMHOVSRVDSITLSMSPQPOPNVILLIDELQ 300
OY 459 YVEKELSEINATAIKSPYNT--VTGLAGAIYVEQVARTVAGYGRYSGKMFQETMEAE 516
DB 301 YVEKELSEINATAIKSPYNT--VTGLAGAIYVEQVARTVAGYGRYSGKMFQETMEAE 360
OY 517 YOTSIOEKPLITIGSSAGLVFLIIVAVIATYCN--RGEFEADSYTYKLDHYTSGHATP 575
DB 361 YOTSIOEKPLITIGSSAGLVFLIIVAVIATYCN--RGEFEADSYTYKLDHYTSGHATP 420
OY 576 GKKITIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKXREIFVA 635
DB 421 GKKITIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKXREIFVA 480
OY 636 IKTLKSGYTEKORDELSEASIMCOFHPNVIHLEGVYTKSTPYMITTEPMENGLSDSFL 695
DB 481 IKTLKSGYTEKORDELSEASIMCOFHPNVIHLEGVYTKSTPYMITTEPMENGLSDSFL 540
OY 695 RNDGQFTVIOLVGLRGIAGMKYVLADMNVYHRDLAARNITLVNSNYCVKSDGSLRFL 755
DB 541 RNDGQFTVIOLVGLRGIAGMKYVLADMNVYHRDLAARNITLVNSNYCVKSDGSLRFL 600
OY 756 EDDTSDPFTYSLGCKPIRMTAPEATQYRKFTSASVWSYGVIMVEMVSGERPYWDMT 815
DB 601 EDDTSDPFTYSLGCKPIRMTAPEATQYRKFTSASVWSYGVIMVEMVSGERPYWDMT 560
OY 816 NQDYIMALEDDYRLPPMDCPALQMLDQWCKDRHNRKFGQIVTLTKMIRNPSTLK 875
DB 661 NQDYIMALEDDYRLPPMDCPALQMLDQWCKDRHNRKFGQIVTLTKMIRNPSTLK 720
OY 876 AMARLSSGINPLDRTIPDFTSPNVDMLAIKMGQYKESFANAGFTSFVDVSGQMME 935
DB 721 AMARLSSGINPLDRTIPDFTSPNVDMLAIKMGQYKESFANAGFTSFVDVSGQMME 780
OY 936 DILRVGVTLAGHOKKILNSIOVMAQONQIOSEV 970
DB 781 DILRVGVTLAGHOKKILNSIOVMAQONQIOSEV 815

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CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DB EMBL: U11493; AAA67925.1; --
DB HSSP: P29323; 1B4F.
DB MGI: 104770; Ephb3.
DB InterPro: IPR000719; --
DB InterPro: IPR001090; --
DB InterPro: IPR001245; --
DB InterPro: IPR001426; --
DB InterPro: IPR001660; --
DB InterPro: IPR001777; --
DB Pfam: PF00041; fn3; 2.
DB Pfam: PF00069; pkinase; 1.
DB Pfam: PF00356; SAM; 1.
DB Pfam: PF01404; Eph_Lbd; 1.
DB PRINTS: PRO0014; ENTPBELI.
DB PRINTS: PRO0109; TYRKINASE.
DB PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DB PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DB PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DB PROSITE: PS00790; RECEPTOR_TYR_KIN_V; 1.
DB PROSITE: PS00791; RECEPTOR_TYR_KIN_V; 2; 1.
DB SMART: SM00454; SAM; 1.
DB ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;
DB Transmembrane; Tyrosine-protein kinase.
DB NON_TER
DB FT
DB SQ
Query Match 67.0%; Score 3429; DB 11; Length 938;
Best Local Similarity 68.9%; Pred. No. 5.4e-252;
Matches 653; Conservative 111; Mismatches 166; Indels 18; Gaps 7;
OY 31 EVSGVDEANNPTIRTYQCVNFPSSONMLRTKEIRRGARHIVEMKFSVDCSSIPSY 90
DB 1 EVSGVDEANNPTIRTYQCVNFPSSONMLRTKEIRRGARHIVEMKFSVDCSSIPSY 60
OY 91 GSKETFNLYEADPDSATKTFPNMMEPNVYKVDITADSFQVDGGMKINTFVR 150
DB 61 GSKETFNLYEADPDSATKTFPNMMEPNVYKVDITADSFQVDGGMKINTFVR 116
OY 151 SFGPYSRSGFYAFDQYGGCSLNAVRYFKRCPIRIIONGAIFQETLSGASTSVLA 210
DB 117 SFGPYSRSGFYAFDQYGGCSLNAVRYFKRCPIRIIONGAIFQETLSGASTSVLA 176
OY 211 SCIANAEVDYDIKLYCGDGEMLVPIGRMCCKAGFEAVENGITVCRGCPSTFAN 270
DB 177 ACIANAEVSVPLKLYCNGDGEMLVPIGRMCCKAGFEAVENGITVCRGCPSTFAN 236
OY 271 ACTHCPINSRTTSEGATNCVCRNGYRADLDPLDMPCTTIPSAPOAVISSVNETSL 330
DB 237 PCLPCPPNSRTTSPASISCTCHNNFYRADSDSACTTTRSPRGVINSVNETSL 296
OY 331 TPBRSGGREDLVNIIICKSGSGRGA-----CTRCGDNVOYAPQOLGTEPRYIS 385
DB 297 TPBRSGGREDLVNIIICKSGSGRGA-----CTRCGDNVOYAPQOLGTEPRYIS 356
OY 386 AHOTYTFEIQAVNGVTDQSPSPFASVNIITNQAPSAVSIMHOVSRVDSITLSMSP 445
DB 357 AHOTYTFEIQAVNGVTDQSPSPFASVNIITNQAPSAVSIMHOVSRVDSITLSMSP 416
OY 446 DQPNVILLIDELQYVEKELSEINATAIKSPYNT--TGLAGAIYVEQVARTVAGY 503
DB 417 DQPNVILLIDELQYVEKELSEINATAIKSPYNT--TGLAGAIYVEQVARTVAGY 474
OY 504 SGKKYFQMTTE-AEYQTSIOEKPLITIGSSAGLVFLIIVAVIATYCNRGERADSE 562
DB 475 THREFFETTSBERSGAQDQLEQPLIVGSAVAFVEMVVAVIALCKORRGPDAEY 534
OY 563 DKLDHYTSGHATPDKLQYTKSTPYMITTEPMENGLSDSFL 622
DB 535 EKLQDY----IAGMKYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEV 590

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QY 623 HLKLPGRKREIFAIAKTLTKSGYTEKORDFLSEASIMGOFDHPNVIHDEGVYTKSTPVMII 682
QY 591 RLKLPGRREVEVAIKTLTKVYTERKORDFLSEASIMGOFDHPNVIHDEGVYTKSRPVMII 650
QY 683 TEFMENGSLDSFLRONDQFTVIOLVGMRLGIAAGMKYLADMTVYHRDLAARNLVNSL 742
QY 651 TEFMENGALDSFLRONDQFTVIOLVGMRLGIAAGMKYLSMNTVYHRDLAARNLVNSL 710
QY 743 VCKVSDFLSRLLEDPTSDPTYSALGKRPRIWTAPEAIQYRKFTSASDVWSYGIWME 802
QY 711 VCKVSDFLSRLLEDPTSDPTYSALGKRPRIWTAPEAIQYRKFTSASDVWSYGIWME 770
QY 803 VMSYGERPYMDTNOVDYNALIEDYRLPPMDSCSALHQLMLDCWQKDRNHPKFGQIVN 862
QY 771 VMSYGERPYMDTNOVDYNALIEDYRLPPMDSCSALHQLMLDCWQKDRNHPKFGQIVN 830
QY 863 TLDMKIRNPNLSIKAMAPLSSGINPLDRTIPDTYSFTVDEMELAIKMGYKSEFANAG 922
QY 831 TLDMKIRNPNLSIKAMAPLSSGINPLDRTIPDTYSFTVDEMELAIKMGYKSEFANAG 890
QY 923 FTSFVDSQMMEDILIRVGVTLGAGHOKKILNSIQYRAQMNQISVEY 970
QY 891 FASFDLVAAQMTADLIRISVTIVGHOKEKILCSIDMRLOMOTLPVQY 938

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RESULT 4
QYH2V4 PRELIMINARY; PRT; 983 AA.
AC 09H2V4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE EPHRIN RECEPTOR EPHA3 COMPLETE FORM.
GN EPHA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RA Chiari R., Hames G., Stroobant V., Maille B., Texier C., Mach B.,
RA Boon T., Coulle P.G.;
RT "Identification of a tumor specific shared antigen derived from an
RT Eph-receptor and presented to CD4 T cells on HLA class II molecules.";
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF213459; AAG43576.1; -.
KW Receptor.
SQ SEQUENCE 983 AA; 110130 MW; BE04DBF958245424 CRC64;

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Query Match 57.08; Score 2917.5; DB 4; Length 983;
Best local Similarity 57.28; Pred. No. 4.9e-213;
Matches 550; Conservative 170; Mismatches 221; Indels 21; Gaps 12;
QY 6 EETLMDSTTAAELGKMWHPSPGMEVSGYDENMNTIRTYOVNVSESSONMLRTKFIK 65
QY 29 EVNLIDSKTIOGELGWTISYSHGMEISGVDEHTPIRTIYOVNVMDHSONMLRTKMWVP 88
QY 66 RGAHRIHVEKESVSRDCSSIPSVSGCKETPNLIYIYEAQFDSATKTFPMENPVMKVD 125
QY 89 RNSAQKIYELKFTLRDCNSIPVLGTCETFNLYMESDDHGVK---FREHOFKID 144
QY 126 TIAADESQVDLGGRYMKINTEVRSFGVPSRSGEYLAFOYDGCGMSLIAVAFYKRCPR 185
QY 145 TIAADESTQMDLDRILKLTETELREVGPVAKKGFYLAFOYDGCVALVSVRYFKKCP 204
QY 186 IIONGAIFQETLSGAESTSLVAAGSCIANAEVDPPIKLYCNGDEMLVPIGCKMAG 245
QY 205 TVKNLAMPDVP-MDSQSLVEVSGSVNNSKEEDPP-RMYCSTEGEMLVPIGCKSCNAG 262
QY 246 FEAVENGTVCGKCSGRTCAAGDBACTHCPINSTRITSSEGTNCVNGRYRARDLDCDM 305

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DB 263 YE--ERGFMCQACRPFYKALDGNMCKACPPHSSFQEDGCSMNCENNYFRADKDPSPM 320
QY 306 PCTTISAPQAVISSVNETSLMEWTTPPDSCGRELVNITICKSCGSRGACTRCGNV 365
DB 321 ACTRPPSSPRNVISNINETSVIDMSWPLDTGGRKDYFNITICKKCGMNIKCEPCSPV 380
QY 366 QYAPROLGTEPRITSDLAHQYFEEIOAVGVDSQFSPFOPASVNTITNOAPSAV 425
QY 381 RLPDROGLNTVTVYDILAHNTYFEIDAVNGVSELSPPROFAVSIITNOAPSPV 440
QY 426 SIMQVSRVDSITLWSOPDPNGVILDYLOIYKELESEYNATRIKS-PIN-TVTGLK 483
DB 441 LTIKORTSNTSLSWOBEHPNGIILDEYVYKOEQETSSTYLIRARGINVTISLK 500
QY 484 AGAIYVQVARKVYAGIGRSGCMYFOTMEAEYQNSIOEKPLIIGSSAAGLVFLAVY 543
DB 501 PDIYVQIARAKAAG:GINSRKFEEETSPDS-FSISGESQVYMLAISAAVAILLTIV 559
QY 544 VIAIV--CNRGRPERADSEYTDKLOHYTSGH-TFGMKIYIDPTFYEDPNEAVERFAKE 599
DB 560 IYVLIGRFGCKSKRGAD----EKRLHFGHILKPLGLRTYVDPHTYEDPTQAVHEFAKE 615
QY 600 IDISCVKIEQYIGAGEFGEVCSGHLKLPKREIFAIAKTLTKSGYTEKORDFLSEASIMG 659
DB 616 IDATNISIDKVVAGAGEFGEVCSGRLKPSKKEISVALTKTLKVTTEKORDFLSEASIMG 675
QY 660 QFDHPNVIHLEGVYTKSTPVIITFEFMENGSLDSFLRONDQFTVIOLVGMRLGIAAGMK 719
DB 676 QFDHPNVIHLEGVYTKSTPVIITFEFMENGSLDSFLRONDQFTVIOLVGMRLGIAAGMK 735
QY 720 YLADMTVYHRDLAARNLVNSNLVCKVSDFLSRLLEDPTSDPTYSALGKRPIMWTA 779
DB 736 YLSMGVYHRDLAARNLVNSNLVCKVSDFLSRLLEDPTSDPTYSALGKRPIMWTA 793
QY 780 EAIQYRKFTSASDVWSYGIWMEVSGYGERPYMDTNOVDYNALIEDYRLPPMDSCSAL 839
DB 794 EAIQYRKFTSASDVWSYGIWMEVSGYGERPYMDTNOVDYNALIEDYRLPPMDSCSAL 853
QY 840 HOLMLDCWQKDRNHPKFGQIVNTLDMKIRNPNLSIKAMAPLSSGINPLDRTIPDTYS 899
DB 854 YQLMLDCWQKDRNHPKFGQIVNTLDMKIRNPNLSIKAMAPLSSGINPLDRTIPDTYS 913
QY 900 NTVDEMELAIKMGYKSEFANAGFTSPDVVSQMMEDILIRVGVTLGAGHOKKILNSIQVR 959
DB 914 RTTGWMLGVWTAHCKELFTGEVYSSCDTIKISTIDMKKGVTVVGPQKKIISITALE 973
QY 960 AQ 961
DB 974 TO 975

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RESULT 5
QYH4H4 PRELIMINARY; PRT; 552 AA.
AC 09H4H4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE DJ74M1.1.1 (TYROSINE KINASE ISOFORM 1) (FRAGMENT).
GN EPHB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RA Baaguley C.;
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AN035704; CAC10350.1; -.
KW kinase.
KW NON-TER
FT SEQUENCE 552 AA; 62206 MW; D643D1C857B1A3DB CRC64;

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Query Match 55.1%; Score 2818.5; DB 4; Length 552;
 Best Local Similarity 99.1%; Pred. No. 6.3e-206;
 Matches 547; Conservative 1; Mismatches 1; Indels 3; Gaps 2;

422 PSANVIMHOVSRTVDSITLSMSQDPDQNGVILDELYEYKEKELSEVNATAIKSPNTVT - 480
 1 PSANVIMHOVSRTVDSITLSMSQDPDQNGVILDELYEYKEKELSEVNATAIKSPNTVT 60

481 -GLKAGAIYFVOVRATVAGYGRYSGKMFQMTTEAYOTSTIOEKLPLIIGSSAGLVFL 539
 61 OGKAGAIYFVOVRATVAGYGRYSGKMFQMTTEAYOTSTIOEKLPLIIGSSAGLVFL 120

540 IAVVAIYVGN-RRGERADSETTDKLOHTSGHTTPGKITYIDPTTYEDPNEAVREFAK 598
 121 IAVVAIYVGNRRRGERADSETTDKLOHTSGHTTPGKITYIDPTTYEDPNEAVREFAK 180

599 EIDISCVKIEQVIGAGEFEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLSEASIM 658
 181 EIDISCVKIEQVIGAGEFEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLSEASIM 240

659 GQPDHPNVHLLEGVYTKSPVMIITEFMENGSLDSFLRQNDQGFYIQLVGMRLGIAAGM 718
 241 GQPDHPNVHLLEGVYTKSPVMIITEFMENGSLDSFLRQNDQGFYIQLVGMRLGIAAGM 300

719 KYLADNNVYHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTYSALGKFPRIKMTA 778
 301 KYLADNNVYHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTYSALGKFPRIKMTA 360

779 PEAIQYRKFTSASDVWSYGIYVMEVWSYGERPYWMTNODVINAIEODYRLPPMDCCPSA 838
 361 PEAIQYRKFTSASDVWSYGIYVMEVWSYGERPYWMTNODVINAIEODYRLPPMDCCPSA 420

839 LHQLMDCQOKDRNHRPRKFGQIVNTLDKMI RNPNLSLKAAAPLSSGGINPLDRTTIPDYS 898
 421 LHQLMDCQOKDRNHRPRKFGQIVNTLDKMI RNPNLSLKAAAPLSSGGINPLDRTTIPDYS 480

899 FNTVDEMLEIAIKMGQYKESFANAGFTSFVVSQMMEDILRGVTLAGHOKKILNSIOVM 958
 481 FNTVDEMLEIAIKMGQYKESFANAGFTSFVVSQMMEDILRGVTLAGHOKKILNSIOVM 540

959 RAQMOIOSEV 970
 541 RAQMOIOSEV 552

RESULT 6
 O9H4H3 PRELIMINARY: PRT: 621 AA.
 ID O9H4H3:
 AC O9H4H3:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE DJ74M1.1.2 (TYROSINE KINASE ISOSFORM 2) (FRAGMENT).
 GN EPHB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Baguley C.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL035704; CAC10351.1;
 KW kinase.
 FT NON_TER
 SO SEQUENCE 621 AA; 69824 MW; 3DA4A10CEB04979BF CRC64;

Query Match 55.0%; Score 2814.5; DB 4; Length 621;
 Best Local Similarity 99.1%; Pred. No. 1.6e-205;
 Matches 546; Conservative 1; Mismatches 1; Indels 3; Gaps 2;

422 PSANVIMHOVSRTVDSITLSMSQDPDQNGVILDELYEYKEKELSEVNATAIKSPNTVT - 480
 1 PSANVIMHOVSRTVDSITLSMSQDPDQNGVILDELYEYKEKELSEVNATAIKSPNTVT 60

481 -GLKAGAIYFVOVRATVAGYGRYSGKMFQMTTEAYOTSTIOEKLPLIIGSSAGLVFL 539
 61 OGKAGAIYFVOVRATVAGYGRYSGKMFQMTTEAYOTSTIOEKLPLIIGSSAGLVFL 120

540 IAVVAIYVGN-RRGERADSETTDKLOHTSGHTTPGKITYIDPTTYEDPNEAVREFAK 598
 121 IAVVAIYVGNRRRGERADSETTDKLOHTSGHTTPGKITYIDPTTYEDPNEAVREFAK 180

599 EIDISCVKIEQVIGAGEFEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLSEASIM 658
 181 EIDISCVKIEQVIGAGEFEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLSEASIM 240

659 GQPDHPNVHLLEGVYTKSPVMIITEFMENGSLDSFLRQNDQGFYIQLVGMRLGIAAGM 718
 241 GQPDHPNVHLLEGVYTKSPVMIITEFMENGSLDSFLRQNDQGFYIQLVGMRLGIAAGM 300

719 KYLADNNVYHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTYSALGKFPRIKMTA 778
 301 KYLADNNVYHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTYSALGKFPRIKMTA 360

779 PEAIQYRKFTSASDVWSYGIYVMEVWSYGERPYWMTNODVINAIEODYRLPPMDCCPSA 838
 361 PEAIQYRKFTSASDVWSYGIYVMEVWSYGERPYWMTNODVINAIEODYRLPPMDCCPSA 420

839 LHQLMDCQOKDRNHRPRKFGQIVNTLDKMI RNPNLSLKAAAPLSSGGINPLDRTTIPDYS 898
 421 LHQLMDCQOKDRNHRPRKFGQIVNTLDKMI RNPNLSLKAAAPLSSGGINPLDRTTIPDYS 480

899 FNTVDEMLEIAIKMGQYKESFANAGFTSFVVSQMMEDILRGVTLAGHOKKILNSIOVM 958
 481 FNTVDEMLEIAIKMGQYKESFANAGFTSFVVSQMMEDILRGVTLAGHOKKILNSIOVM 540

959 RAQMOIOSEV 969
 541 RAQMOIOSEV 551

RESULT 7
 O73875 PRELIMINARY: PRT: 987 AA.
 ID O73875:
 AC O73875:
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE EPH-LIKE RECEPTOR TYROSINE KINASE RTK5.
 OS Brachydanio rerio (zebrafish) (Zebrafish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbortinae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cooke J.E., Xu Q., Wilson S.W., Holder N.;
 RT "Characterisation of five novel zebrafish Eph-related receptor
 RT tyrosine kinases suggests roles in patterning the neural plate."
 RL Dev. Genes Evol. 206:515-531(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX PubMed-11171340;
 RA Cooke J.E., Moens C.B., Roth L.W.A., Durbin L., Shiom K., Brennan C.,
 RA Kimmel C.B., Wilson S.W., Holder N.;
 RT "Eph signalling functions downstream of Val to regulate cell sorting
 RT and boundary formation in the caudal hindbrain."
 RL Development 128:571-580(2001).
 DR EMBL: AJ005026; CAA06299.2;
 DR InterPro: IPR000719;
 DR InterPro: IPR001090;
 DR InterPro: IPR001245;
 DR InterPro: IPR001660;

QY	66	RGRAHRIIVEKFEVRCRCSIFSPVSCSKETPNLYXYEADFDATATPFPMNMENPNVAVD	125
Db	91	RDGARVYAEIKFTLRRCNMSNPVLYGCKKETFPNLYXYESDRDLGASr---QDSQFLKLD	146
QY	126	TIADDESFOYDLCGRVAKITEVRSFGVYRSRGFYIAFODYCGMSLAVRVFYKCRP	185
Db	147	TIADDESFTGADLCVRRLKLTMTVEVRSGLPSKRGFYLAFODIACTALATSLRTYKKCPA	206
QY	186	IIIONGATFOEHLGAESESTLVAAAGSGSIIANAEEVDYIKLYCNGDGEFWLVPICRCKAKG	245
Db	207	WVRNLAFSELVATDSSLSLEVNGQCVRISEEDTP-KATCSAEGEMLVPTCKYCSAG	265
QY	246	FEAVENGTVRCGCSGTGFEKANOGDEACTHCPINSRITPSEGATNCVCVCRNGYTRADLPDM	305
Db	266	YE--ERRDACVACELGFRYKSPAGDQLCARCPRHSHSAAPAAQACHDLSYRAALDPSS	323
QY	306	PCTITPSAPPAVVISVNETSILMELMTPPRSGCHEDLVYNIICKSCSGSGAGACTRCGDNV	365
Db	324	ACTRPPSPAVNLISVNGTSTLTLEMARLPDGGSDITTYNAVCRRCWALSREACSGSGT	383
QY	366	QYAPROLGCTPEPRYISDLNHTYTEFIOAVNVNTDQSPFSPOFASVNTTNOAAPSAV	425
Db	384	RFYVQQTSLVQASLVANLALAHMYSTWIEEVKNVSDLSBPRAAVNTTNOAAPSVQ	443
QY	426	SIMHQVSTVDSITFLSMSODPQNGVILDELOYEKELSEYNATAIKSPTN--TVTGK	483
Db	444	VVIRORERAGQTSVSLTMOEPPQPGIITLEYEIKRYEKDEKQMSYSTLKAVTATRAVSGLK	503
QY	484	AGATVYPOVARYATVAGVGRYSGKKRPTQ--MTAEKQTSIOEKLPTITLSSAAGLVFLI	540
Db	504	PGTRVFEVYVARTSAGGCRFSQAAVELEGKRPRIYRTIYIJCLLTIG-----L	554
QY	541	AVVVAIAVCNRR--GFERADSEYDKLDQHYTSG-----HTTQGM---KIYIDP	584
Db	555	VYLLLLLLCKRHGQYSAPGDDSEKIMHONQOAPRVFLRLHNHPRGKLPREQVNERH	614
QY	585	TYEDPNEAVREPAKEIDISCYKIEQVIGAGEFEGVCGSHLKECKREIEFAIKTLASGT	644
Db	615	TYEEBGRGSRFTRIETESRIHIEKIIIGSGDSEVCGRILVPOQROVPVALAKAKGYT	674
QY	645	EKORPDFLSEASIMQOPHPVNIHLEGVYKSTVMTIITEPFEMNGSLDSEFLRQNDQGFV	704
Db	675	ERORPDFLSEASIMQOPHPVNIHLEGVYKSTVMTIITEPFEMNGSLDSEFLRQNDQGFV	734
QY	705	IOLVGLMLGIAAGKYYLADNMVYVHRDLAARNILVNSMLVCVSDSFLSRELEDDETDPY	764
Db	735	MOLVGLMLGIAAGKYYLADNMVYVHRDLAARNILVNSMLVCVSDSFLSRELEDDETDPY	793
QY	765	TSALGCRKPIWTAPEALQYKRTFSASVNSYUGIVMNEVNSYGBRPPQMDMTNDVNAIE	824
Db	794	TWT--GKPIPIWTAPEALQYKRTFSASVNSYUGIVMNEVNSYGBRPPQMDMTNDVNAIE	852
QY	825	QDYRLPRPMDCPSPALHQLMLCMQKDRNHRKFCQIOWTLIDKMLRNPNLSIKAMAPLSGI	884
Db	853	EGYRLPRPMDCPSPALHQLMLCMQKDRNHRKFCQIOWTLIDKMLRNPNLSIKAMAPLSGI	911
QY	885	NLPLDLRTIPIQYTSN-----TYDEMLAIKMQQYKESFANAGFTSFDVYSQAMMDIL	938
Db	912	PPAPVRCFCFDRGSGGGGGLYTGWDWLSIRMGYRDBHFAAGGYSLGLVLRNMADVR	971
QY	939	RGVGTFLAGHOKKILNSIGVMAQMNQIQ	966
Db	972	ALGITLMGHOKKILNSIGVMAQMNQIQ	999
RESULT	9		
ID	073879	PRELIMINARY;	PRT; 880 AA.
AC	073879;		
DT	01-AUG-1998 (Tremblrel. 07, created)		
DT	01-AUG-1998 (Tremblrel. 07, last sequence update)		
DT	01-MAR-2001 (Tremblrel. 16, last annotation update)		
DE	EPH-LIKE RECEPTOR TYROSINE KINASE TRK4 (FRAGMENT).		

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GN      RTK4.
OS      Brachydanio rerio (zebrafish) (Zebrafish) (Zebrafish).
OC      Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC      Cypriniformes; Cyprinidae; Rasbora; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Cooke J.E.;
RL      Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Cooke J.E., Xu Q., Wilson S.W., Holder N.;
RL      Dev. Genes Evol. 206:515-531(1997).
CC      -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN
CC      TYROSINE PHOSPHATE (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC      RECEPTOR SUBFAMILY.
CC      -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC      EMBL, AJ005030; CAA06303.1; -.
CC      DR      HSSD; P00523; 2PRT.
CC      DR      ZFIN; ZDB-GENE-990415-61; rtk4.
CC      DR      InterPro: IPR0000561; -.
CC      DR      InterPro: IPR0000719; -.
CC      DR      InterPro: IPR001090; -.
CC      DR      InterPro: IPR001245; -.
CC      DR      InterPro: IPR001426; -.
CC      DR      InterPro: IPR001660; -.
CC      DR      InterPro: IPR001777; -.
CC      DR      Pfam; PF000041; fn3; 2.
CC      DR      Pfam; PF00069; kinase; 1.
CC      DR      Pfam; PF01404; EPH_Lbd; 1.
CC      DR      PRINTS; PR00014; FNTYPE11.
CC      DR      PRINTS; PR00109; TYRKINASE.
CC      DR      PROSITE; PS01186; EGF_2; UNKNOWN_1.
CC      DR      PROSITE; PS00197; PROTEIN_KINASE_ATP; 1.
CC      DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC      DR      PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC      DR      PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
CC      DR      PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
CC      DR      SMART; SM00219; Tyrc; 1.
CC      KW      ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;
CC      Transferase; Transmembrane; Tyrosine-protein kinase.
CC      FT      NON_TER      1
CC      FT      NON_TER      1
SQ      SEQUENCE      880 AA: 98862 MW: 8875013FBI79B70B CRC64;

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[illegible]

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OY 331 TPRDSGSGREDLVYNIICKSCSGRGACTRCGDNYOAPAROLGTEPRYISDLAHTOY 390
   || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 294 SPPLASGGRODLTYNVVYCKVBDTRGCPGDVAVYSQRLSTSTRSVHQLAHTNY 353
OY 391 TREIQAQVAVTQSPSPSPASVNTTNOAPSAVSIMHOVSRTVDSITLSQDPDQNG 450
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 354 TFOIVAVNVSCKHNSPEQAVSVTLTNOAPSVMWSVOSKIDTRITLALFWDOEKPNK 413
OY 451 VILDEYAEKELEFYNATKSPNT--VITGAKAGAIYVOVARATAGVGRSGKMY 508
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 414 VILEEVKYEEDQNRSTRIYKTSRNADIDLPPLSYVHVARRARAGGDSAPPE 473
OY 509 FQTMF-EAEYQTSIOEKLPLIIGSSAAGVFLIYAVVIAIVCNRGFERADESYTDLOH 567
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 474 FSTNVAAAPVGVMSNAVLLLVAGCVVLLLIIFPITIKRR-----SKYS-KTKQ 526
OY 568 YTSGHITPCKIYIDPFYEDPNEAVREFAKEIDISCKVIEOYIAGGEVCSHLKIP 627
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 527 GEDKNVQGVRIYVDFYEDPNOAIRFAKEINTSCIKIEKVIIGIGEVCVSGRLKIP 586
OY 628 GKREIFVAIKTSGYTERKORDFLEASIMGOPHPNVIHLEGVYKSTPYMITTEPME 687
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 587 GKREICVAIKTKAGFTBQRDLFSEASVIGQFHPNIIHLEGVYTKCKPVMITTEPME 646
OY 688 NSLDSFLRNDQOFTVIOVLGMLRGIAAGMKYLAIDMNVHBDLAARNILVSNLVCKYS 747
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 647 NSLDMFLRKNDCRFTVIOVLGILRGIASGMKYLSDMSVYHBDLAARNILVSNLVCKYS 706
OY 748 DGLSRLEDDSDPTYSALGCKFPRIWTAPEAOYKFTSASVWSGTYMWEVMSYG 807
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 707 DGMKSRVLEDE-PEGAYTYTR-GGKIPIRMTAEALTIRKFTSASVWSGTYMWEVMSYG 764
OY 808 ERPYDMTNOYINAEIDYRLPPMDCPSALHQLMLDCMQRNHRPRKFGQIVATLTKK 867
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 765 ERPYDMSNQDYTKALIESGYRLPPMECPALHQLMLCEMMEHRRDRKFSQIVAMDKL 824
OY 868 IRNPSKLAMAPLSSGICNLPILDKRTIPDYT--SEPTVDEWLEAIKMGYKESFANA 921
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 825 IRNPATLTKTAGASRSHPTINHAPSECSASPLASVDMLKILGLEQYRENFNTA 880

RESULT 10
OY 073878 PRELIMINARY; PRT; 976 AA.
AC 073878;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
DE EPH-LIKE RECEPTOR TYROSINE KINASE KTK8.
GN KTK8.
OS Brichy'danio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Cooke J.E., Xu Q., Wilson S.W., Holder N.;
RL Dev. Genes Evol. 206:515-531(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Durbin L., Brennan C., Shioml K., Cooke J., Barrios A.,
RA Shanmugalingam S., Guthrie B., Wilson S., Lindberg R., Holder N.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ005029; CA006302.1; -.
DR HSP: P00523; 2PTK.
DR ZFIN: ZDB-GENE-990415-65; rtk8.
DR InterPro: IPR000561; -.
DR InterPro: IPR000719; -.
DR InterPro: IPR001090; -.
DR InterPro: IPR001245; -.
DR InterPro: IPR001660; -.
DR InterPro: IPR001777; -.

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DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; kinase; 1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF01404; EPH_1cd; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD001495; -. 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR SMART; SM00454; SAM; 1.
DR ATP-binding; EGF-like domain; Glycoprotein; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 976 AA; 108180 MW; 4619754A38BBD01F CRC64;

Query Match 52.3%; Score 2674; DB 13; Length 976;
Best Local Similarity 54.5%; Pred. No. 1.66-194;
Matches 529; Conservative 164; Mismatches 245; Indels 32; Gaps 16;

OY 1 LLAAYEELMNSTITATLGMVHHPSC--WEVSGYDEMNTIRTYOVNVESSQNN 57
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 LVSAEEVLMNTKLETSDLRWITV-PSGDPEMEGSDGDEGNSVRFQYCPM-DSSVSH 77
OY 58 WLRTKFIIRRGARHIVMKFSVRDCSSIPSPGCKETFMUYEADFDSATFTFPMM 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 WLRTKFIIRRHASQVYVIRFTMMECSAMPASFRCKETFMUYEADFDSATHTAPMM 137
OY 118 ENPVKVDITIADESEFQVLDGRVYMKINTEVRSFPGVSRSGFYLAPODYGGCSLIAVR 177
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 138 ENPVSKVDVTADEFLRR---GGERKSNVKTVRGPLSLGFYLAPODYGCAMALLSVR 193
OY 178 VEYRCRPTIONGAIPOETLSGASTSLV-AARGSTIANAE---EVDPILKYONGGGEW 233
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 194 VEFKCPAVSAFSEFPTL---PHSLVQAGVGVNDSAPFQCTAPPMFGEDGQW 249
OY 234 L-VPIGRCMKAGFEAVENGTVCRGCPSTFKANQDGEACTHCPINSTRYSEGAIVCYR 292
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 250 VGPSTSTACAPGEVPVSDR-CRACGLGQYKASVGSGLCVCPDNSNTHSAGSSLCYR 308
OY 293 NGYRADIDPLDMCCTTPSPAPQAVISSVNETSLMLEMTPPRDSGGRBDLYNIICKSCG 352
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 309 PGYHRTASDLPDSACTYKPPSPARSIITQINDTVTLEMSPLDGRGSDLSYSVECHMC- 367
OY 353 SGRGA-CYRGGDNOYAPROLGTEPRYISDLAHTOYPEIQAQVNDQSPSPQFA 411
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 368 --RSSLVCQCADSTIRYRGQMGVSGRYITKGLPHTYITFTVLAQNGVSAVSHTPASS 425
OY 412 SVNITNOAPSAVSIMHOVSRTVDSITLSWSQDPQNGVILDEYQYEKELSE-YNAT 470
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 426 SVNITTSRDVAVPVGIRIKASSSSVISWTVPRPOHSDIOQLYSLKGGODGMQYV 485
OY 471 AIKSPNTVTGLKAGAIYVOVARATYAGGRYSGKMYFQTMFEAEYQTSIOEKLPLIG 530
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 486 SSRSSVYVLDLSRAQYOYQVVARATYAGGHFSSAVSISTLPDDESSP---RLMLTGV 542
OY 531 SSAAGVFLIYAVVIAIVCNRGFERADSEYTDLOHTYSGHITPCKIYIDPFYEDPN 590
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 543 LVATGLILIAVVIYVFCFRSTRTRRDPD-PDKSGOFLMQO--GIKVIIDPFYEDPN 598
OY 591 EAVREFAKEIDISCVKTEOYIAGGEFEVCSGHLKIPGKREIFAIAITLKSGETERORD 650
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 599 EAVREFAKEIDISVYKTEOYIAGGEFEVCSGHLKIPGKREIFAIAITLKGTTDKORD 658
OY 651 FLASASTMGQFDHPNVIHLEGVYKSTPVMITFEMENGLDSEFLRNDQOFTPIOLVGM 710
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 659 FLSEASIMGQFOHPNIHLEGVITASCVMILTEYMEGALDSEFLRLNDQOFTPIOLVGM 718
OY 711 LRGTAAAGKYTIADNIVYHRLAARNILVNSNLVCKVSDFLSRLEDDSDPTYSALG 770
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 719 LRGTAAAGKYTISESVYHRLAARNILVNSNLVCKVSDFLSRLEDDSDPTYSALG 778
OY 771 KPIRMTAPEAIOYRKFTSASDVWSYGIWMWEVMSYGERPYMDTNOYINAEODYRLP 830

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Db	779	KIP1PMTAPBEAIAFRKFTSASDVSYGIWMVEVMSFCGRFPYWMKSNQDYINAIHQDYRLP	838
Qy	831	PMDCPSALHQLMLDCKWOKDNHNRPKRGQIYNTLDKMITRPNLSLKAAAPLSSGGINPLD	890
Db	839	PPPECPASLHQLMLDCKWOKERSRRPCATVSAIDRLIRNPASIKITGRIPDPGSPHLLD	898
Qy	891	-RTIDYVSFNTVDMEFLAIKMGQYKESFNAVAGTSFSDVYSQMMEDILRWGVTLAGHOK	949
Db	899	ORAPPLSHSCSSVADWMLRAIMERYEDAFWQAGTATQIHITHISTEDLKIIGVTLAHHOK	958
Qy	950	KILNSIQVMR 959	
Db	959	KILNSVQTLR 968	
RESULT	11		
ID	Q9P269	PRELIMINARY; PRT; 853 AA.	
Q9P269			
AC	Q9P269;		
DT	01-OCT-2000 (TREMblrel.15, Created)		
DT	01-OCT-2000 (TREMblrel.15, Last sequence update)		
DT	01-MAR-2001 (TREMblrel.16, Last annotation update)		
DE	KIA1459 PROTEIN (FRAGMENT).		
GN	KIA1459.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID:9606;		
RN	[1]		
RA	SEQUENCE FROM N.A.		
RA	MEDLINE-20277482; PubMed-10819331;		
RT	Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;		
RT	"Prediction of the coding sequences of unidentified human		
RT	genes. XVII. The complete sequences of 100 new cDNA clones from brain		
RT	DNA Res. 7:143-150(2000)."		
RL	DNA Res. 7:143-150(2000).		
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN		
CC	TYROSINE PHOSPHATE (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN		
CC	RECEPTOR SUBFAMILY		
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.		
DR	EMBL; AB040892; BAA93963.1; -.		
DR	InterPro; IPR000561; -.		
DR	InterPro; IPR000719; -.		
DR	InterPro; IPR001245; -.		
DR	InterPro; IPR001426; -.		
DR	InterPro; IPR001660; -.		
DR	InterPro; IPR001777; -.		
DR	Pfam; PF00041; fn3. 2.		
DR	Pfam; PF00069; pkinase. 1.		
DR	Pfam; PF00536; SAM. 1.		
DR	PRINTS; PR00014; FNTYPEIIT.		
DR	PRINTS; PR00109; TYRKINASE.		
DR	PROSITE; PS01166; EGF_2; UNKNOWN.1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP. 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM. 1.		
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR. 1.		
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1. 1.		
DR	PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2. 1.		
DR	SMART; SM00060; FN3. 1.		
DR	ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;		
DR	transferase; Transmembrane; Tyrosine-protein kinase.		
KW	NON_TER		
Q0	SEQUENCE 853 AA; 94149 MW; 7248501BFB855002 CRC64;		

Query Match	45.6%	Score 2332;	DB 4;	length 853;
Best Local Similarity	51.7%	Pred. No.1.4e-168;		
Matches 446;	Conservative 153;	Mismatches 221;	Indels 42;	Gaps 12
QY	132	SFSQVLDGGRVAKITFVNSFGPVSHSGCYLAFQDYGGCGLIAVNFYRKCRRIITONGA	191	

Dd	1	SEFGADGLVRLKLTINTEVRSVGP:LSKRGKGFVAPDIDGACIALIILSTRITYYKKCPAMVNNLA	60
Oy	192	IFQETLSGAESTSLVAARGSCIANAEEDVPIKLYCNGDEBMLVIGRCCKAGFEAVEN	251
Dd	61	AFSEAVTGTADSSSLVEVNGQCVRLHEERDTP-KMYCSAEGEMVLPICKYCSAGYE--ER	117
Oy	252	GTVCRGCGSSGTFKANGODEACTHCPINSRTTSEBATWCYCRNGRYRADDDPLDMPCTTIP	311
Dd	118	RDACVACELGKYKSAKPGDQLCARPPHSHSAAPAAQACHDSLSTYRALDPPSACIRP	177
Oy	312	SAPQAVISEVNETS:LMLEMPRPGSGREDLVNMIICKSGSGAGACTRGDNVQVAPRO	371
Dd	178	SAPVNLISVNGTSYTLLEMARPPDPPGRSDITTYAAYCRRCRPMALSRCEACSGSTRVPOQ	237
Oy	372	LGTEPRILYDLTAHQTYTEFIOAVNGVYDOSDPFQASVNTITNOAPSAVSIHQV	431
Dd	238	TSLVQASLLVANLLAHMYSFWIEAVNGVSDLPSEPRAAVNTITNOAPSOQVVIROE	297
Oy	432	SRVYDSTILMSOPDQNGVLYDELOYEKELESEYNAATIAKSPTN--TYTGKACAIY	489
Dd	298	RAGOTS:SLLMQEEPOPGILLLEYEIKYEIKDKMOJSTYLKATWTRATVSGLKGPTRY	357
Oy	490	FOVRRATVAGYGRYSCKMKYFOT---MTEAEKOTSIOEKLPLITIGSSAAGLVPLIAVVA	546
Dd	358	FOVRRATSAGCGRRSQAMEVETGKPRPRYDRTITVWICLLITIG-----LVYLLL	408
Oy	547	IVCNRR--GFERADSEYTDKLOHYTSG-----HITPGM---KIYIDPFYEDPN	590
Dd	409	LICKRHGYSKARODSDSEKMHYONGQARPPVPLPLPHHPGKLRPEQFYAOPHTYDEPG	468
Oy	551	EAVREFAKEIDISCVKIEQVYAGAEFEYVCSGHLKLRGKEIFALYTLKSGTTEKORD	650
Dd	469	RAGRFETREIDASRIHEKIIIGSDSDSEYCGRI:RVGGRVPAFALAKAGATYERORD	538
Oy	651	FLSEASINGOEDHPVHILEGVNKKSPVMIITEFMENGSLDPSLRONDOQFYIOYVGM	710
Dd	529	FLSEASINGOEDHPHRIIRLEGVYTRGRGLAMVITYEMNGSLDTFLKTHDOQFTIMQLVGM	588
Oy	711	LRGIAAGMKYIADNMVYHRLDAAANIILVNSNLVCKVSDPGLSRPLEEDTSDPTYTALG	770
Dd	589	LRGVAGAGRYLSDIGYVHRLDAAANVLVDNSLVCKVSDPGLSRVLEDD- PDAAYTTT- GG	646
Oy	771	KPFIPTAPPAIIOYRKFTSASDVWSYGIWMEVMSYCEPRYMDTNDQVYNALEBODYRLP	830
Dd	647	KIPIKMTPEBIAIERTFSSASDVWSFGVYMEVYLAZERPMYMNNTNDVYISVEEGRLP	706
Oy	831	PPMDCPSALHOLMDCMQKDNHNRPKFGQIYNTLDKMIHNPNSLKKAAAPLSSGNIPLLD	890
Dd	707	APMGCPSALHOLMDCMQKDNHNRPKFGQIYNTLDKMIHNPNSLKKAAAPLSSGNIPLLD	890
Oy	891	RTIPDYTSFN-----TVDEMLEAIKKGQYKESFANAGFTSFVDVSOAMMEDILRYGVTL	944
Dd	766	RSCFDLRGSGSGGGGLTYGMDLDSIRMGRRYNDHFAAGYSLSGVNLMNNOVDYRALGITL	8255
Oy	945	AGHQKILNLSIQVRAQMOHQIQ 966	
Dd	826	MGHOKKILGSIOTMRAOLTSTO 847	

RESULT	12	
Q9PMR5		
ID	Q9PMR5	PRELIMINARY; PRT; 977 AA.
AC	Q9PMR5;	
DT	01-MAY-2000 (TREMBUREL, 13, Created)	
DT	01-MAY-2000 (TREMBUREL, 13, Last sequence update)	
DT	01-MAR-2001 (TREMBUREL, 16, Last annotation update)	
DE	EPH RECEPTOR TYROSINE KINASE PRECURSOR.	
GN	EPHA2.	
OS	Xenopus laevis (African clawed frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;	
OC	Xenopodinae; Xenopus.	

OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99077686; PubMed-9858686;
 RA Hebling P.M., Tran C.T., Brandt A.W.;
 RT "Requirement for EphA receptor signaling in the segregation of Xenopus
 third and fourth arch neural crest cells."; Mech. Dev. 78:63-79(1998).
 RL Mech. Dev. 78:63-79(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
 TYROSINE PHOSPHATE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 RECEPTOR SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBROBLASTIN TYPE III-LIKE DOMAINS.
 DR EMBL: AJ002493; CA05500.1; -
 DR HSPSP; P08631; IAD5.
 DR InterPro: IPR000561; -
 DR InterPro: IPR000719; -
 DR InterPro: IPR001090; -
 DR InterPro: IPR001245; -
 DR InterPro: IPR001426; -
 DR InterPro: IPR001660; -
 DR InterPro: IPR001777; -
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF01404; EPH_1bd; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRODOM: PD001495; -; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR SMART: SM00454; SAM; 1.
 DR AT-Blinding: Glycoprotein; Kinase; Phosphorylation; Receptor; Signal;
 KW Transferrase; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 977 EPH RECEPTOR TYROSINE KINASE.
 FT SEQUENCE 977 AA; 109593 MW; 9931C19031A55F1D CRC64;

Query Match 45.0%; Score 2300.5; DB 13; Length 977;
 Best Local Similarity 48.2%; Pred. No. 4.4e-166;
 Matches 463; Conservative 161; Mismatches 313; Indels 23; Gaps 14;

QY 1 LLAAYETLMDSTVATYAEIGMNVHP-PSGWEEVSGYDENMNTIRTYOVCNVESSQNNML 59
 Db 22 VLOREVVLLDEKQTQGLGMLTHPYGKGMILLQNV-MNGSLITYVCSVQEGQDNWL 80
 QY 60 RTKFLRRGARHRIHEMFVSVDSSISVPSCKETNLYYEDEPSATITFFNMEN 119
 Db 81 RTNMLYRSEAGLIEFLKFTYVDCNSFPGSGCTCKETNLYMESDIDYGT---NFKR 136
 QY 120 PAVKVDITAADESFQVLDGRVYKINTEVRSFGVSSGFLAQQDGGCSLIAVRVF 179
 Db 137 QPKRIDITAPDDITVPAPFASRNKVNVEKRSYGALSKGFLAQQDGGCSLIAVRVF 196
 QY 180 YRCKPRTIIONGAIFQETISGAESTSLVARSGSCIANAEV--DVEIKLYCNGDEMLVPI 237
 Db 197 YKCPVYVQAGMAQFPEIYVAGADSGIAKVSCKVNNAVSVNDDP-TJHCNNDGEMLVPI 255
 QY 238 GRCKKAGFEAVENCTVGRGCPSTGTFKANOGDEACTHCPINSTRISSEATNCVANGYYR 297
 Db 256 GHCLQPGYEV--GDTQACQPGFYSKTSNGPCQLPDHTEPSSQAATPCPCNDGFR 313
 QY 298 ADIDPDMPTTIPAPQAVISVNETSLMEWTPPRDSGGREDLVYNIICKSCSGSGA 357
 Db 314 STDPSSDPCTSPFASRDLTAVDGSKVLMRLPSPNSGGRSDITTYVTEKCKAPSE 373
 QY 358 CTCRCGN-VQYAPROLGLTEPRIYISDLAHTQYTFEIQAVNGVDGSPSPQFASVIT 416

Db 374 CTPODHSNIRESENPJELKGTITIMDLEPHLNTSFTEARNVSG-SGSSRSYATLRIS 432
 QY 417 TNQAPPASVSIHVOYSKRVDSITLSMSQPDQNGIILDEYQYER-ELSEYNATAISP 475
 Db 433 INQTEPPVYVTEFTLNDQSTLSMSVPPROQTRWAKTEYYSKHDANSISVQRCGN 492
 QY 476 TINTVGLKAGAVIYQVAVARTVAGRGSKMYEQTMTAEAYOTSIOEKLPLIGSSNAG 535
 Db 493 SVTLKLKPLGTYTVVAVQALQDEGVGYSRDEYFEFTLVEE-----SSNKAIVIGALAG 547
 QY 536 LVELLAVVIAIVCNKRQFERADSEYTKLOHTYSGHITTPGKTIYIDPFTTEDEAVRE 595
 Db 548 SI-IIAIFGVYIIFMRRRRNPINIRHSESDIYFSKPDOLKPLKTYVDHTYEDPKKAVLK 606
 QY 596 FAKEDISCVKIEQYVIGAGEVCSGHLKIPGKEITVAIKTKSGYTEKORRDLSEA 655
 Db 607 FTMRPRTPSRKAKVIGAGEVEVFKGLKLPKKESTVAIKTKLAGTTEKORRDLSEA 666
 QY 656 SIMGQFDHPNVTHLEIYVTKSTPVMIITEFMENGLSDSFLQNDGQFTVQLVGLRGIA 715
 Db 667 SIMGQFCHNIIRLES-WSKYPKMIIVTEHMEENGALDKFLKNDGSEFSPQLVGLRGIA 725
 QY 716 AGKYLADMTYVHRDLAARNILVNSLVCKVSDGSLRFLDDTSDPYTSALGCKPFR 775
 Db 726 AGKYLSEMYVHRDLAARNILVNSLVCKVSDGSLRFLDDTSDPYTSALGCKPFR 783
 QY 776 WTAPPAIYRKFTSADVWSYGIWMEVMSYGERPYMTNODVYNALTEQDRIPLPPMD 835
 Db 784 WTAPPAIYRKFTSADVWSYGIWMEVMSYGERPYMTNODVYNALTEQDRIPLPPMD 843
 QY 836 PSALQLMLDCQKDRNRPFGQIVNTFLDMIRNPSLKKMAPLSSGJNPLDRTIPD 895
 Db 844 PSAILQLMLDCQKDRNRPFGQIVNTFLDMIRNPSLKKMAPLSSGJNPLDRTIPD 903
 QY 896 YTSFNTVDEWTEAIKAGYKSSPANAGFTSPDVVSQMMEDILRYGVTLAAGHOKILNSI 955
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RESULT 13
 ID 09Y1J0 PRELIMINARY; PRT; 1080 AA.
 AC 09Y1J0;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE EPH RECEPTOR TYROSINE KINASE.
 GN EPH OR DEK OR CG1511.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99286310; PubMed-10356296;
 RA Scully A.L., McKeown M., Thomas J.B.;
 RT "Isolation and characterization of Dek, a Drosophila eph receptor
 protein tyrosine kinase."; Mol. Cell. Neurosci. 13:337-347(1999).
 RL EMBL: AF132028; AAD38508.1; -
 DR HSSP: P00523; 2PTK.
 DR FLYBase: FBgn0025936; Eph.
 DR InterPro: IPR000561; -
 DR InterPro: IPR000719; -
 DR InterPro: IPR001090; -
 DR InterPro: IPR001245; -
 DR InterPro: IPR001660; -
 DR InterPro: IPR001777; -
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR Pfam: PF01404; EPH_1bd; 1.

PRINTS: PR00109; TYRKINASE.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS0107; PROTEIN_KINASE_ATP_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM_1.
 DR PROSITE; PS0109; PROTEIN_KINASE_TYR_1.
 DR SMART; SM00454; SAM; 1.
 DR ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
 KW SEQUENCE 1080 AA; 121505 MW; 314DC3322DC2C89 CRC64;

Query Match 39.68; Score 2028; DB 5; Length 1080;
 Best Local Similarity 42.18; Pred. No. 2.8e-145;
 Matches 440; Conservative 162; Mismatches 322; Indels 120; Gaps 26;

QY 2 LAAEETLMDSTTATLAEGLMWHVH-----PSGMEVSGYD-ENMNTIRTYQVCNFEES 53
 Db LAHDOVLLDTREATLEMTREYRPGQAQTPGWNESFTDFVGIMN-RSYVVCDAVYH 137
 QY 54 SONMMLRTKTRRRGAHINHEMKFSVRDCSSIPSVSCKETENLYYEADPFSAKTF 113
 Db NVNMNLSMSPFIDRGSANLTYEIOFTINDCSLFGNMLSCKETSLFYE--FDAATREP 195
 QY 114 PMNENPMVKYDTIADES-FSQ--VDLGRVAKINTEVSRFGVSRSGFYLAPODYG 169
 Db PPMQTDSTRLRIARAGGRNONSVD-----INTEVKSIA-VNKKGYEFPRQGA 247
 QY 170 CMSLIARVRYRCKPRRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 229
 Db CISVLAAYVYITCPAVTENFAHNETPTGREITIEKQNGCTVDNAEPYETPYL-CKG 306
 QY 230 DGEMLVPIGRMCKAGFEAVENGVCRCGSPGTFKANGDEACHHCINSTTSEGATNC 289
 Db DGMTITLGGCRCKAGTEPNTNKTCECPGTSEKSEVTK-CPRCPPNSAKSXTGSPFC 365
 QY 290 VCRNGYRADLPDLMCTTIPSAF-QAIVSSVNETSLMLEWTPRRDSG----- 338
 Db KCAGGYRHPMDGRHMCYSPAPATNLTLFVQDTSAIISMSPANKNESSTSTNKIY 425
 QY 339 REDLVYNIKSCSGSGRACRCGDNYQVAPRGLGTEPRIYSDDLAPHQYFETIOAVN 398
 Db HSDIVYKI-----KCNICSPNVVYNPSDPTFNETKITLNLPRVYTYVQIHAIN 475
 QY 399 GVTQSPSPFQ-----ASVNTITNOAPSAVS 426
 Db SVSHINEFKRHSNSSLVANSVDFVSTSLNLPDLNEVKTAGAEVFTTESVLLSTVP 535
 QY 427 IMHOVSTVDSITLWSOPDPNGVILDELYQYER-ELSEYNATAI-KSPNTVTGLK 483
 Db NLRILATINNDADLEMDKPVQSDPDLFEYERMPKVELDAINKSALNTRKETAHIVGL 595
 QY 484 AGATVVOVARATVAGYGRYSGKMYFOTME--AEQYTSIQEKLPLITGSSAGLVPLIA 541
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 QY 542 VVYIAVCNRRGERADESEYTKLQHTSGH-----TP---CMKIYIDPFY 586
 Db FIATVYEMR-----SKHODDLKSTNHLPLPLDYASNEVTPPLFGNSRSVDPHTY 706
 QY 587 EDPREAVREPAKELEDISCVKIEQYIAGEGEVCSGHLKPGK-REIYVAITLNSGYT 644
 Db EDPQQAIREAREIDANYITIEAIIIGGEGEDVCGRRLKIPRPFVQDIDVAITLKGSS 766
 QY 645 EKORADLFSASIMGDFHNVHLEGVTKSPVMTITFEMNGSIDSLRONDQFTV 704
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 QY 705 IQLVGLRGIAAGMKYLAADNVYHRLAARNILVNSNLVCKVSDFGSLRELEDDTDPY 764
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 QY 765 TSLAGGFFPRMTPAPLQYRKETSADWSYGVIMAEWVSIEGEPYMDTNDQVINAIE 824
 Db TTR-GGKIPRMTAPALIAIRKFTSADWSYGVIMAEWVSIEGEPYMDTNDQVINAIE 943

QY 825 QDRLPPMPCPSALHOLMLDCMOKDRNHRPKFQGIYNTIDKMTIRPNSLKAMAPLSSGI 884
 Db KGYLPPMPCPSALHOLMLDCMOKDRNHRPKFQGIYNTIDKMTIRPNSLKAMAPLSSGI 1003
 QY 885 NLPLDRITPDYTSFNVDLEAIKMGQYKESFANAGTSPFVDSQMMEDILRVGVTL 944
 Db GNHILDCQ-RGQNFIFSTDLMEHIKMSRCHHEKANLNLAQISLRTMOQLSDMKTIL 1062
 QY 945 AGHOKITLNSQVWRQMOQISV 968
 Db VGHOKITLH-----QAROLDIT 1079

RESULT 14
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 AC Q917D4,
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE EPH PROTEIN
 GN EPH OR CG1511.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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 RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
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 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mikhina N.V., Modarity C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weisslock G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195 (2000).
 DR EMBL; AE003843; AAC21122.1;
 DR InterPro; IPR000561;
 DR InterPro; IPR000719; -


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OY 290 VCRNGYRADLDPDMCTTIPSAP-QAVISSVNETSLMLEMTPPRDSG-----338
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OY 339 REDLVYNIICKSCSGRGACTRCGDNQYAPRQLGTPEPRYISDLAHTOYTFEIOAVN 398
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Db 415 SVSHINEFKRHSNSSLVAVSDIVFSNNTSLNIPDLNENKVGQAEIVFTTESVLSTVF 474
OY 427 IMHQVSRVDSITLSKSPDPQNGVILDELOYE-----KELSEYNATAI--KSPNT 478
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OY 537 VELLAUVVIAVCRNGEERADSEYTDKLQHTYSCHI-----TPGMK--578
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OY 579 -----IYIDPFYEDPNEAVREPAKEDISCVKIEQVGTAGEFEGYCSGHLK 625
Db 641 HLANTTPLFGNSRKYVPHTYEDPNQAIREFARIDANVTITIEAIIGGEGFVDCRGRLK 700
OY 626 LPGA--REIFVAIKTTLKSGYTEKORRDLSEASIMGFDPHPNVILHLEGVYTKSTPVMIIT 683
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Job time: 207 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2001, 16:29:39 ; Search time 23.96 Seconds

(without alignments)
2454,310 Million cell updates/sec

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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 412676

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Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	970	100.0	970	16	AA1985089
2	587	60.5	1055	21	AA19591
3	480	49.5	987	21	AA19590
4	322	33.2	994	16	AA19590
5	322	33.2	994	18	AA19590
6	103	10.6	995	16	AA19590
7	103	10.6	1011	16	AA19590
8	77	7.9	77	21	AA19590
9	40	4.1	998	16	AA19590
10	40	4.1	998	17	AA19590
11	39	4.0	59	14	AA19590

12	39	4.0	59	16	AA195924
13	37	3.8	57	16	AA195911
14	37	3.8	57	19	AA195917
15	37	3.8	57	20	AA195914
16	36	3.7	57	16	AA195907
17	35	3.6	973	16	AA195908
18	35	3.6	988	16	AA195910
19	35	3.6	990	15	AA195899
20	35	3.6	993	16	AA195843
21	35	3.6	993	16	AA195844
22	32	3.3	951	16	AA195704
23	31	3.2	360	16	AA195667
24	31	3.2	380	14	AA195612
25	31	3.2	849	16	AA195706
26	31	3.2	972	16	AA195668
27	31	3.2	972	17	AA195631
28	31	3.2	984	14	AA1954513
29	31	3.2	986	16	AA195936
30	31	3.2	986	16	AA195091
31	31	3.2	987	16	AA195963
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37	29	3.0	40	16	AA195896
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ALIGNMENTS

RESULT 1
AA195089
AA195089 standard. Protein: 970 AA.
AA195089:
16-APR-1996 (first entry)
EPH-like receptor protein tyrosine kinase HEK5.
EPH-like receptor protein tyrosine kinase; PTK; HEK5;
human eph-like kinase; therapy; diagnosis; vector; antibody.
Homo sapiens.
W09528484-A1.
26-OCT-1995.
14-APR-1995: 95WO-US04681.
15-APR-1994: 94US-0229509.
(AMGE-) AMGEN INC.
Fox GM, Jing S, Welcher AA;
WPI: 1995-373799/48.
N-PSDB; AAT02946.
New nucleic acid encoding EPH-like receptor tyrosine kinase(s)
and related vectors, host cells, proteins, antibodies etc., used
diagnostically and therapeutically to modulate receptor activation
or prodn.

Protein tyrosine-k
Human receptor typ
Receptor protein t
Receptor protein t
Eph-related PTK Ce
Eph-related PTK Ce
Eph-related PTK Ce
Human embryonal ki
Protein p140 CDNA
Protein p140 CDNA
Non-differentiated
Elk PTK. Rattus r
Eph-related PTK Ce
Mature non-differe
Full-length recept
alk. Rattus ratu
Protein tyrosine-k
EPH-like receptor
Human non-differen
Protein tyrosine-k
Full length recept
Receptor type tyro
Receptor-type tyro
PTK gene Hprt5 pro
EPH-like receptor
Eph-related PTK Ce
Eph-related PTK Ce
Eph-related PTK Ce
Receptor protein t
Receptor protein t
Mouse Bsk receptor
Rat Rsk7 eph-relat

XX Claim 18; Page 46-49; 133pp; English.

PS 4 Novel human Eph-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (AA02946-49) from a human fetal
 CC brain cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken Eph-like receptors Cerk5, Cerk7 and Cerk8.
 CC HEK11 shows no homology to any known Eph-like receptor. Recombinant
 CC HEK11 receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host
 CC cells, and are used to produce antibodies (utilised in diagnostic
 CC assays), or to identify and purify ligands for HEK receptors, or
 CC therapeutically to modulate the activation of cell-associated
 CC receptors. Soluble HEK5 receptor may affect primarily brain and
 CC pancreatic cells.

XX Sequence 970 AA:

SO Query Match 100.0%; Score 970; DB 16; Length 970;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 841 qumlcqwckdrhrrkfgqiyvltlckmirnpsnlkamaplssgilpldrtipydtsfn 900

OY 901 TVDEMLEAIKMOYKESFANAGFTSPDYVSQMMEDILRVGVTLAGHOKILNSIQVRA 960
 DB 901 tvdeMLEAIKmqykesfanagftspdyvsqmmmedilrvgvtlaghqkllnsiqvra 960

OY 961 QMNQIQSVYV 970
 DB 961 qmnqisvvev 970

RESULT 2
 AAB19591
 ID AAB19591 standard; Protein: 1055 AA.
 XX
 XX AAB19591;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 DE Human CASB616.
 XX
 XX CASB616; EPHB2; ERK; EPH3; EPH73; DRT; HEK5; EPHB2V;
 KW receptor protein tyrosine kinase; human; antigen; colon cancer;
 KW ovary cancer; autoimmune disease; vaccine; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200053216-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 28-FEB-2000; 2000WO-1P01587.
 XX
 PR 05-MAR-1999; 99GB-0005124.
 XX
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Vinals De Bassols YC.
 XX
 DR WPI: 2000-587384/55.
 DR N-PSDB: AAA8549.
 XX
 PT Vaccine composition for treating ovarian and colon cancer, comprises
 PT CASB616 polypeptides, polynucleotides or antigen presenting cells
 PT expressing the polypeptides
 PS
 PS Claim 1; Page 42; 57pp; English.

XX The present sequence is that of human CASB616, a member of the Eph
 CC and Eph-related family of receptor protein tyrosine kinases.
 CC CASB616 is also known as EPHB2, ERK, EPH3, EPH73, DRT, HEK5 and
 CC EPHB2V. CASB616 polypeptides and polynucleotides are important
 CC immunogens for specific prophylactic or therapeutic immunization
 CC against tumours, especially colon cancer (claimed) and ovarian
 CC cancer. They are specifically expressed or highly over-expressed
 CC in tumours compared to normal cells and can thus be targeted by
 CC antigen-specific immune mechanisms leading to destruction of the
 CC tumour cells. They can also be used to diagnose the occurrence of
 CC tumour cells. Their inappropriate expression can also cause an
 CC induction of autoimmune responses, which can be corrected through
 CC vaccination using the CASB616 polypeptides or polynucleotides.

XX Sequence 1055 AA:

Query Match 60.5%; Score 587; DB 21; Length 1055;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 967; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

1 LLAAVEETLMDSTATAELGMVHPPSGWEVSGYDENMNTIRTYQVGNVFESSQNMWLR 60
 15 llaaveetlmdstataelgmvhppsgweevsgydenmntlirtygvcnvfessqnmwlr 74

61 TKEIRRRGAHRIHVEKFEVRDCSSIPSPVSGCKEFTFNLYYEADPDSATKTFPMWMMNP 120
 75 tkfirrrgahrihvekfvrdcssipspvsgckeftnlyyyeadpdsatktfpwmwnmp 134

121 WKVVDTLADESFQVLDLGRVWKINTEVRSRSGEVLAFQDYGCSMLIAVRVY 180
 135 wkvvdtdlaadesfqvldlgrvwmkintevrsrsgevlafqdygcsmliavrvy 194

181 RKCPRITONGAIFOEFLSGAEESTSLVAARGSCIANAEVDPRIKXCGDGEMLVPIORC 240
 195 rkcpriiongafioeflsgaeestslvaargscianaeedvprikxcgdgemplvpiorc 254

241 MCKAFPEAVENGTCVRCGPSTGFKANQDDEACTHCPINSRTTSEGATNCVCRNGYRADL 300
 255 mckafpeavengtcvrcgpstgfkangddeacthchpinsrttsegatncvcrngyradi 314

301 DPLDMPCTTPSAPQAVISSVNETSLMEPTPPRDSGREDLVNIIICKSCGSGRACR 360
 315 dpldmpcttspapqavissvnetslmleptpprdsgrredlvnyilickscsgsgracr 374

361 CGDNQVAPROGLTEPRITVYISDLAHTQYTFEIOAVNGVVDOSFSPQFASVNTINNOA 420
 375 cgdnvqaproglteprityisdlahatqytfelioavngvvdosfspqfasvntinnoa 434

421 APSASIMHOVSRYVDSITLMSQDPDPNGVILDELOYEKELSEYNATAIKSPNTVT 480
 435 apsasimhovsryvdsitlmsqdpdpngvildeloyekelseyynataikspntvt 494

481 --GLKAGAIYFQVAFARVAGYGRSGKMYQMTAEVQOSTOEKPLITIGSSAALVF 538
 495 vglkagailvyfqrarvavagyrsgkmyqmtaeqvostoeekplitigssaalfvf 554

539 LIAVVAVIATVNCNRGFERADSEYTDKLQHYTSGHITPQMKIYIDPTVEDPNEAVREFAK 598
 555 liavvaviatvncnrgeradseytdklqhytsghtpkmkiyidptvedpneavrefak 614

599 EIDISCVITEOVIGAGEGECVSGHLKPKRETFVAIKTLKSYTEKORRDLSEASIM 658
 615 eidiscviteovigagegecvsghlkpkretfvaiktlksytekorrdlseasim 674

659 GQDPHPVNIHLEGVYTKSTPYMITTEFMENGSLDSFLRQNDGQFTVTOVGMLRGIAAGM 718
 675 gqdp HPVNIHLEGVYTKSTPYMITTEFMENGSLDSFLRQNDGQFTVTOVGMLRGIAAGM 734

719 KYLADMYVNRDLAARNILVNSNLVCVSPFGLSRFLIEDTSDPTTYTSAALGKFPRIWTA 778
 735 kyladmyvnrldlaarnilvnsnlvcvspfglsrfliedtspdpttytsaalgkfpriwta 794

779 PEALIOYRKFTSASDVMSTGYIWMVEVNSYGERPYWDMTNOVINAIEDVDYLPMPMCCPSA 838
 795 pealioyrkftsasdvmsstgyiwmvevnsygerpywdmtnovinaiedvdylpmpmccpsa 854

839 LHQMLDCKMCKDRNHRPKFCQIYVNTLDKMTIRNPNSLKAMAPLSSGSLNPLLDRTTIPDYS 898
 855 lhqml dckmckdrnhrpkfcqi yvntldkmtirnpnslkamap lssgslnplldrttipdys 914

899 FNTVDLEWLEIKKGOYKESFANAGFTSPDVVSQMMEDILRVGVTLAGHOKKILNSIQVA 958
 915 fntvdelewleikkgoyk esfanagftspdvvsqmm edilrv gvtlaghokkilnsiqva 974

959 RAQMNOIQSVE 969
 975 raqmnoiqsve 985

RESULT 3
 AAB19590
 ID AAB19590 standard; Protein: 987 AA.
 XX
 AC AAB19590;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Human CASB616.
 XX
 KW CASB616; EPHB2; ERK; EPH3; EPH3; DR1; HEK5; EPHB2V;
 KW receptor protein tyrosine kinase; human; antigen; colon cancer;
 KW ovary cancer; tumour; autoimmune disease; vaccine; therapy;
 XX
 OS Homo sapiens.
 XX
 XX
 Key Location/Qualifiers
 FT Misc-difference 568..569
 FT /note- "an additional Arg residue decodes from the
 FT CASB616 nucleotide sequence given in the
 FT specification (see AAB8548), but is not
 FT given in the CASB616 amino acid sequence in
 FT the specification"
 FT Misc-difference 956
 FT /note- "encoded by GTT"
 FT
 PN WO200053216-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 28-FEB-2000; 2000WO-BP01587.
 XX
 PR 05-MAR-1999; 99GB-0005124.
 XX
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Vinals De Bassols VC;
 XX
 DR WPI: 2000-587384/55.
 DR N-PSDB; AAB8548.
 XX
 PT Vaccine composition for treating ovarian and colon cancer, comprises
 PT CASB616 polypeptides, polynucleotides or antigen presenting cells
 PT expressing the polypeptides
 XX
 PS Claim 1: Page 41; 57pp; English.
 XX

The present sequence is that of human CASB616, a member of the EPH and EPH-related family of receptor protein tyrosine kinases. CASB616 is also known as EPHB2, ERK, EPH3, EPH3, DR1, HEK5 and EPHB2V. CASB616 polypeptides and polynucleotides are important CC immunogens for specific prophylactic or therapeutic immunization CC against tumours, especially colon cancer (claimed) and ovarian CC cancer. They are specifically expressed or highly over-expressed CC in tumours compared to normal cells and can thus be targeted by CC antigen-specific immune mechanisms leading to destruction of the CC tumour cells. They can also be used to diagnose the occurrence of CC induction of autoimmune responses, which can be corrected through CC vaccination using the CASB616 polypeptides or polynucleotides.
 CC
 XX
 SQ Sequence 987 AA;

Query Match 49.5%; Score 480; DB 21; Length 987;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LLAAVEETLMDSTATAELGMVHPPSGWEVSGYDENMNTIRTYQVGNVFESSQNMWLR 60
 15 llaaveetlmdstataelgmvhppsgweevsgydenmntlirtygvcnvfessqnmwlr 74

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OY 61 TKFIRRGARHRIHVEKKFSVRDCSSIPVSGCKETFNLYYEADFDSATKTFPMNMENP 120
DB 75 LKfIIRgahrIhVemkIsVrDCSSIPVsgCKetfNfLyYeAdFdSaTkTfPmNmEnP 134
OY 121 WVKVDTIAADESFQVDLGGRWKINTFEVRSFQVSRSGFYLAFODYGCMGLIARVRFY 180
DB 135 WVKVDTIAADESFQVDLGGRWKINTFEVRSFQVSRSGFYLAFODYGCMGLIARVRFY 194
OY 181 RKPFRITQNGAIFQETLSGAESISVAARGSCIANEEDVPIKIKYCNQDGMVLPIGRIC 240
DB 195 RKPFRITQNGAIFQETLSGAESISVAARGSCIANEEDVPIKIKYCNQDGMVLPIGRIC 254
OY 241 MCKAGFEAVENGTVCRGCGSGTFKANOGEACTHCPINSRTTSEGATNCVANGYRADL 300
DB 255 mckAgfeAvengTvcRgcGsgTfKAnoGeActhCpInsrTtSegatncvAngyRadl 314
OY 301 DPIDMECTITPSAPQAVISSVNTSIMEWTTPRDSGREDLYNITICKSGSGRGACTR 360
DB 315 dPIDmECTITPSApQAVIssvNtSiMEwTTPrDSgREDlyNITICKSGSGRGACTR 374
OY 361 CGDNVOYAPRQLGLTFEPRYISDLAHTQYTFEIQAVNGVTDOSPPSPQFASVNTTNOA 420
DB 375 cGdnVoyApRqLgLTfEPryISdLAHTQyTFEIqAVNGvTDOsPPSPqFASvNTTNOA 434
OY 421 APSAVSIMHOVSRTVDSITLWSQPDOPNGVITLDYEQYTERKLSFYNNATIKSPNTVT 480
DB 435 aPSaVSIMhOVsRtVdSiTLwsqPdOpNgViTlDyEQyTERkLSfYNNAtIKsPnTvt 494

```

RESULT 4

AAR87018 standard; Protein; 994 AA.

AAR87018:

19-MAR-1996 (first entry)

Receptor tyrosine kinase (neural kinase).

Receptor tyrosine kinase; neural kinase; Nuk; axon;

axogenesis; nerve disorder.

Mus musculus.

Location/Qualifiers

Peptide

Region

Region

Region

Region

Region

Region

Region

Region

Region

Region

Region

Region

Region

Region

Region

Region

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XX (MOUN ) MOUNT SINAI HOSPITAL CORP.
PA Henkemeyer M, Letwin K, Pawson A;
XX WPI: 1995-393299/50.
XX N-PSDB: AAT07308.
XX DNA encoding neural receptor tyrosine kinase - useful in gene
XX therapy of nerve disorders, and for diagnosis and identification of
XX therapeutic agents
XX Claim 1, Page 70-74; 103pp; English.
XX A novel receptor tyrosine kinase (AAR87018), designated neural kinase
XX (Nuk) (AAR87018), is encoded by cDNA (AAT07308) obtd. from a mouse
XX embryo library. Nuk is expressed in migrating axons and is
XX involved in cell-cell interactions and axogenesis in development
XX of the nervous system. Nuk or its fragments (pref. amino acids
XX 26-548 or 601-994) are used to identify (ant.)agonists of the
XX (activated) receptor tyrosine kinase as a means of treating nerve
XX disorders and damage, or to raise antibodies used to monitor axon
XX migration and nerve cell interactions.
SQ Sequence 994 AA:

```

Query Match 33.2%; Score 322; DB 16; Length 994;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 159 GFYLAFODYGGCMLIARVFRKCPRIIONGAIROETLSGAESISVAARGSCIANEE 218

DB 181 gFYlAfDyGgCmSlIaRvFrKcPrIiOnGaIRoEtLSgAeSISvAaRgScIaNeE 240

OY 219 VDPYIKLYCNGGEMIVPIGRMCKAGFEAVENGTVCRGCGSGTFKANOGEACTHCPIN 278

DB 241 vDpYIKLyNgGEMiVPIgRmCKAgFeAvengTvcRgcGsgTfKAnoGeActhCpIn 300

OY 279 SRTSEGATNCVCRNGYRADLPLDMPCTITPSAPQAVISSVNTSIMEWTTPRDSG 338

DB 301 srtSegatncvCrNgYradlPlDmPctITPSApQAVIssvNtSiMEwTTPrDSG 360

OY 339 REDLVNITICKSGCGRGACTRCGDNVOYAPRQLGLTFEPRYISDLAHTQYTFEIQAVN 398

DB 361 rEdLVnITICKSGcGrGAcTRcGdnVoyApRqLgLTfEPryISdLAHTQyTFEIqAVN 420

OY 399 GVTDOSPPSPQFASVNTTNOAAPSASVIMHOVSRTVDSITLWSQPDOPNGVITLDYEQ 458

DB 421 gVTDOSPPSPqFASvNTTNOaAPsASvIMhOVsRtVdSiTLwsqPdOpNgViTlDyEQ 480

OY 459 YVEKELSEYNATAIKSPNTVT 480

DB 481 yVeKELsEYnAtaIKsPnTvt 502

RESULT 5

AAW26366 standard; Protein; 994 AA.

AAW26366:

02-DEC-1997 (first entry)

Mouse Nuk tyrosine kinase.

Nuk tyrosine kinase; Eph receptor tyrosine kinase;

signal transduction; axonogenesis; neurodegenerative disease;

Alzheimer's disease; Parkinson's disease; Huntington's disease;

multiple sclerosis; amyotrophic lateral sclerosis;

Wernicke's disease; nerve damage; trauma; ischaemia; stroke.

Mus musculus.


```

OY 574 TPGMKIYIDPFTYEDNEAVREFAKEIDISCVKIEOVIGAGEFGEVCSGHLKPGKREIF 633
   |||||||
Db 599 tpgmklyidpftyeopneavrefakeidiscvkieqyigagetgevcshlkpgkreif 658
OY 634 VAIKTKISGYTERKQRDFTLSEASIMGQFDPHNYIHLEGVVTKS 676
   |||||||
Db 659 valktiksgytekqrdrfdlseasimgqfdhpnvihlegvvtks 701

RESULT 7
AAR75709
ID AAR75709 standard; Protein; 1011 AA.
XX
XX AAR75709;
AC
XX 11-NOV-1995 (first entry)
DT
XX Eph-related PTK Cek5+.
DE
XX
XX Cek5+: Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
XX prognosis.
XX
XX Gallus sp.
OS
XX WO9515375-A.
XX
XX 08-JUN-1995.
PD
XX 07-SEP-1994; 94MO-US10140.
PF
XX 03-DEC-1993; 93US-0162809.
PR
XX (LJOL-) LA JOLLA CANCER RES FOUND.
PA
XX Pasquale EB, Sajjadi FG;
XX
XX WPI: 1995-215256/28.
DR
XX N-PSDB; AAQ90657.
DR
XX
XX Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
PT cancer.
PT
XX
XX Claim 11; Page 71-75; 129pp; English.
XX
XX A cDNA clone encoding a novel variant of Eph-related PTK Cek5,
XX Cek5+ (AAQ90657), was isolated from a chick embryo library in
XX lambda gt11. Cek5+ protein (AAR75709) contains a 16-amino acid
XX insertion in the juxtamembrane domain, and be a result of
XX alternative splicing. Cek5+ is exclusively expressed in the CNS.
XX
XX Sequence 1011 AA;
SQ

Query Match 10.6%; Score 103; DB 16; Length 1011;
Best Local Similarity 100.0%; Pred. No. 1.2e-100; Indels 0; Gaps 0;
Matches 103; Conservative 0; Mismatches 0;

OY 574 TPGMKIYIDPFTYEDNEAVREFAKEIDISCVKIEOVIGAGEFGEVCSGHLKPGKREIF 633
   |||||||
Db 615 tpgmklyidpftyeopneavrefakeidiscvkieqyigagetgevcshlkpgkreif 674
OY 634 VAIKTKISGYTERKQRDFTLSEASIMGQFDPHNYIHLEGVVTKS 676
   |||||||
Db 675 valktiksgytekqrdrfdlseasimgqfdhpnvihlegvvtks 717

RESULT 8
AAB14401
ID AAB14401 standard; Protein; 77 AA.
XX
XX AAB14401;
AC
XX
XX 14-NOV-2000 (first entry)
DT

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XX
DE Mouse ephrin B receptor EphB2 sterile alpha motif (SAM) domain.
XX
XX SAM domain; sterile alpha motif; homodimerisation; heterodimerisation;
XX signal transduction; X-ray crystallography; protein coordinate data;
XX drug development; antibody; T-cell signalling; telomere function;
XX cell proliferative disorder; senescence; ageing; cancer; atherosclerosis;
XX arthritis; angiogenesis; neuronal development; axonal migration;
XX neurodegeneration; neurodegenerative disease; Alzheimer's disease;
XX Parkinson's disease; Huntington's disease; demyelinating disease;
XX multiple sclerosis; amyotrophic lateral sclerosis; nervous system trauma;
XX stroke; ischaemia; cytostatic; immunosuppressive; vulnery;
XX neuroprotective; nocrotropic; antiparkinsonian; cerebroprotective;
XX antiarthritis; antiatherosclerotic; EphB2; ephrin B receptor; murine;
XX receptor tyrosine kinase; mouse.
XX
XX
XX Mus musculus.
OS
XX
XX WO200037500-A1.
XX
XX 29-JUN-2000.
PD
XX 17-DEC-1999; 99MO-CA01209.
PF
XX 18-DEC-1998; 98US-0112929.
PR
XX (MOUN ) MOUNT SINAI HOSPITAL.
PA
XX Stapleton D, Sichert F;
XX
XX WPI: 2000-442645/38.
DR
XX
XX 3-D structure of sterile alpha motif domain used as model for
XX determining 3-D structures of additional native or mutated SAM domain
XX with unknown structure and structures of co-crystals of SAM domain with
XX modulators.
XX
XX Disclosure; Page 60; 72pp; English.
XX
XX The invention relates to the three dimensional structure of a SAM
XX (sterile alpha motif) domain, to peptides (AAB14420-B14525) which mediate
XX SAM domain function, and to potential modulators of SAM domain function.
XX The SAM domain mediates homo- and heterodimerisation and is found in cell
XX surface receptors, cytoplasmic signalling proteins, transcriptional
XX activators and repressors and chimeric human oncoproteins. For example it
XX is present in the Eph family of receptor tyrosine kinases, the
XX transcription factor TEL, members of the polycarb group of
XX transcriptional repressors (e.g., RAR28, Scm), the protein kinase Bcr2p
XX and Liprin scaffolding proteins. SAM domains are therefore thought to
XX play an important role in both normal and oncogenic signal transduction.
XX The X-ray crystal structure was determined for the SAM domain of the
XX murine ephrin A receptor isoform EphA4 (AAB14400; also known as Sek,
XX Sek1, Cek8, Hek8, and Tyro1). The SAM domain corresponds to residues
XX 890-981 of EphA4. The 3D structure of the SAM domain can be used in the
XX determination of the structures of other SAM domain-containing proteins.
XX The SAM domain peptides may be used to identify compounds for drug
XX development and to prepare antibodies. The antibodies can be used to
XX screen for SAM domain-containing proteins, to diagnose and treat
XX disorders associated with aberrant T-cell signalling, and to modulate
XX telomere function. Modulators of SAM domain function may be used to treat
XX diseases associated with inappropriate activity of a protein containing a
XX SAM domain, particularly an Eph receptor. They may be used to treat a
XX cell proliferative disorder such as cancer, atherosclerosis, arthritis
XX and diseases associated with the nervous system, and may be used to
XX modulate angiogenesis. The SAM domain peptides and modulators may be used
XX to modulate the biological activity of an Eph receptor or Eph ligand in a
XX cell, particularly in pathways involved in neuronal development, axonal
XX migration, pathfinding and regeneration. Compositions containing SAM
XX domain modulators may be used in the treatment of neurodegenerative
XX diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's
XX disease, demyelinating diseases such as multiple sclerosis, and
XX amyotrophic lateral sclerosis) and conditions involving trauma and injury
XX to the nervous system (e.g., ischaemia resulting from stroke, and

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CC bacterial and viral infection of the nervous system). The present
 CC sequence represents the SAM domain of murine EphA2.
 XX

Sequence 77 AA:

Query Match 7.9%; Score 77; DB 21; Length 77;
 Best Local Similarity 100.0%; Pred. No. 6, 3e-74;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 894 PDYTSFNTVDEMLFAIKKGOYKESFANAGTSPDVVSQMMEDILRVGVTLAGHKKILN 953
 Db 1 pdytsfntvdeleakikgkfstanagtsfsvsqmmmedilrvgtclagqkkliln 60
 OY 954 SIQVWRAQMNQIQSYEV 970
 Db 61 siqvmraqmqiqsyev 77

RESULT 9
 AAR85092
 ID AAR85092 standard; Protein: 998 AA.

AC AAR85092;

DT 16-APR-1996 (first entry)

DE EPH-like receptor protein tyrosine kinase HEK11.

KM EPH-like receptor protein tyrosine kinase; PTK; HEK11;

KW human eph-like kinase; therapy: diagnosis; antibody; vector.

OS Homo sapiens.

PN W09528484-A1.

PD 26-OCT-1995.

PF 14-APR-1995; 95WO-US04681.

PR 15-APR-1994; 94US-0229509.

PA (AMGE-) AMGEN INC.

PI Fox GM, Jing S, Welcher AA;

DR WPI; 1995-37379/48.

DR N-PSDB; AAT02949.

PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -
 PT and related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation
 PT or prodn.

PS Claim 18; Page 71-75; 133pp; English.

CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal
 CC brain cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cck5, Cck7 and Cck8.
 CC HEK11 shows no homology to any known EPH-like receptor. Recombinant
 CC HEK receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host
 CC cells, and are used to produce antibodies (utilised in diagnostic
 CC assays), or to identify and purify ligands for HEK receptors, or
 CC therapeutically to modulate the activation of cell-associated
 CC receptors.

SO Sequence 998 AA:

Query Match 4.1%; Score 40; DB 16; Length 998;

Best Local Similarity 100.0%; Pred. No. 2, 3e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 775 RWTAPBALQYRKFTSASDVWSTGIVMEVMSYGERPYWDM 814
 Db 801 rwtapealgyrkftsasdvwstgivmewmsysgerpywdm 840

RESULT 10

AAW03421
 ID AAW03421 standard; Protein: 998 AA.

AC AAW03421;

DT 11-NOV-1996 (first entry)

DE Mouse developmental kinase 1.

KM Mouse developmental kinase 1; MDK1; receptor tyrosine kinase; RTK;
 KW signal transduction; probe: diagnosis; therapy;
 KW neurodegeneration; neuroproliferation; cancer.

OS Mus sp.

FT Key Location/Qualifiers

FT Peptide 1..28 /label= Sig-peptide

FT Modified-site 64..66 /label= N-glycosylation_site

FT Modified-site 343..345 /label= N-glycosylation_site

FT Modified-site 410..412 /label= N-glycosylation_site

FT Domain 555..579 /label= Transmembrane-domain

PN W09621013-A1.

PD 11-JUL-1996.

PF 03-JAN-1996; 96WO-US00419.

PR 03-JAN-1995; 95US-0368776.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 (SUGC-) SUGEN INC.

PI Closek T, Millaer B, Ullrich A;

DR WPI; 1996-333988/33.

DR N-PSDB; AAT32960.

PT New mouse development kinase 1 gene - used for developing prods. for
 PT diagnosis and treatment of abnormalities in signal transduction
 PT pathways

PS Example 1; Page 105-108; 128pp; English.

CC Mouse developmental kinase 1 (MDK1) (AAW03421) is a new member of the
 CC eck/eph family of receptor tyrosine kinases (RTKs). Its amino
 CC acid sequence was deduced from a cDNA clone (AAT32960) isolated
 CC from mouse embryo and adult brain libraries. The distinct
 CC patterns of MDK1 expression during mouse development suggest an
 CC important role for MDK1 in the formation of neuronal structures.
 CC MDK1 may be obtd. by expression in host cells. It can be used
 CC in methods for the diagnosis of diseases characterised by
 CC abnormality in a signal transduction pathway, such as
 CC neuroproliferative or neurodegenerative disorders or cancer,
 CC to screen for (ant)agonists, and to raise antibodies.

SO Sequence 998 AA:

Query Match 4.1%; Score 40; DB 17; Length 998;
 Best Local Similarity 100.0%; Pred. No. 2.3e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 775 RMTAPEAIQYRKFTSADVMSYGIYVMEVMSYGERPYNDM 814
 |||||||
 DB 801 rvtapeaiqrkftsdvmsygiyvmewmsygerpyndm 840

RESULT 11

AAR41897
 ID AAR41897 standard; Protein; 59 AA.

AC AAR41897;

DT 10-MAR-1994 (first entry)

DE Partial bptk1 gene prod.

KW PTK; protein tyrosine kinase; catalytic domain; c-kit; brain;
 amplification; primer; polymerase chain reaction; PCR.

OS Homo sapiens.

PN WO9315201-A.

PD 05-AUG-1993.

PF 22-JAN-1993; 93WO-US00586.

PR 22-JAN-1992; 92US-0826935.

PA (NEW-) NEW ENGLAND DEACONESS HOSPITAL.

PI Avraham H, Cowley S, Groopman J, Scadden D;

DR WPI; 1993-320330/40.

PT New protein tyrosine kinase genes and proteins encoded by genes -
 are of human mega-karyocytic origin

PS Claim 7; Fig 9; 60pp; English.

CC PTK genes were identified using two sets of degenerative
 CC oligonucleotide primers: a first set which amplifies all PTK DNA
 CC segments (AAQ49743-44), and a second set which amplifies highly
 CC conserved sequences present in the catalytic domain of the c-kit
 CC subgroup of PTKs (AAQ49745-46). The PTK genes identified are described
 CC in AAQ49747-57 and AAR41897-02.
 CC The bptks are expressed in human brain tissue.

SO Sequence 59 AA;

Query Match 4.0%; Score 39; DB 14; Length 59;
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 733 ARNIIVNSNLVCKVSDFGLSRFLEDDTSPTYSALGK 771
 |||||||
 DB 1 arnlivnsnlvckvsdfgrlfledtsdptysalgrk 39

RESULT 12

AAR85924
 ID AAR85924 standard; Peptide; 59 AA.

AC AAR85924;

DT 14-FEB-1996 (first entry)

XX Protein tyrosine-kinase bptk1 fragment.

KW Protein tyrosine-kinase; PTK; bptk1; agonist; cell growth;
 differentiation.

OS Homo sapiens.

PN WO9527061-A1.

PD 12-OCT-1995.

PF 04-APR-1995; 95WO-US04228.

PR 04-APR-1994; 94US-0222616.

PA (GETH) GENENTECH INC.

PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;

PI Wood WI;

DR WPI; 1995-366160/47.

PT Agonist antibodies which activate specific protein tyrosine
 kinase(s) - also activate chimeric proteins of kinase extracellular
 domain and Ig constant domain, useful for studying, and therapeutic
 modulation of, cell growth and differentiation

PS Disclosure; Page 71-72; 125pp; English.

CC DNA probes based on protein tyrosine-kinase (PTK) sequences were used
 CC to screen cDNA libraries to identify novel PTK genes. The bptks,
 CC bptk1, bptk2, bptk3, bptk4, bptk5 and bptk7 (AAR85924-28 and AAR85935,
 CC respectively) are expressed in human brain tissue and show homology
 CC to known PTKs. These novel PTKs can be used in the design of
 CC drugs that modulate PTK activity.

SO Sequence 59 AA;

Query Match 4.0%; Score 39; DB 16; Length 59;
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 733 ARNIIVNSNLVCKVSDFGLSRFLEDDTSPTYSALGK 771
 |||||||
 DB 1 arnlivnsnlvckvsdfgrlfledtsdptysalgrk 39

RESULT 13

AAR79141
 ID AAR79141 standard; Protein; 57 AA.

AC AAR79141;

DT 22-FEB-1996 (first entry)

DE Human receptor type kinase.

XX receptor type kinase; osteoblast; screening; anti-cancer; diagnosis;
 KW treatment; bone disease.

OS Homo sapiens.

PN JP07155187-A.

PD 20-JUN-1995.

PF 03-DEC-1993; 93JP-0303622.

PR 03-DEC-1993; 93JP-0303622.

PA (ASAH) ASAH KASEI KOGYO KK.

DR WPI; 1995-250736/33.

DR N-PSDB; AAQ96250.


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XX Human receptor tyrosine kinase partial cDNA - used to develop
PT medicaments for the treatment of bone disease caused by
PT proliferation of osteoblast cells
XX
XX Claim 1: Page 5; 5pp; Japanese.
PS
CC The human receptor tyrosine kinase was isolated from a human
CC osteoblastoid cell line (MG63) by reverse transcriptase-polymerase
CC chain reaction. The gene fragment (AA096249) can be used for the
CC screening of cells for anti-cancer agents, and for treatment of bone
CC diseases due to the proliferation of osteoblasts.
XX
SQ Sequence 57 AA:

Query Match 3.8%; Score 37; DB 16; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.4e-31;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 735 NILVNSNLVCKVSDPGLSRFLEDDTSDPTYSALGK 771
Db 1 nilvnsnlvckvsgdfglrflddtsdptysalqgk 37

RESULT 14
AAW79147
ID AAW79147 standard; Protein: 57 AA.
XX
AC AAW79147;
XX
DT 19-NOV-1998 (first entry)
XX
DE Receptor protein tyrosine kinase (PTK) subtype tyro-5.
XX
KM PTK; receptor; protein tyrosine kinase; brain tissue.
XX
OS Rattus sp.
XX
PM US5811516-A.
XX
PD 22-SEP-1998.
XX
PF 02-JUN-1995; 95US-0456647.
XX
PR 15-MAY-1992; 92US-0884486.
PR 02-MAY-1994; 94US-0237401.
PR 02-JUN-1995; 95US-0456647.
XX
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI Lai CHC, Lemke GE;
XX
DR WPI: 1998-530939/45.
DR N-PSDB; AAV55890.
XX
PT Receptor protein tyrosine kinase polypeptide, tyro-3 - preferably
PT expressed in brain tissue
XX
PS Example 2: Columns 45-46; 46pp; English.
XX
CC This represents a novel receptor protein tyrosine kinase (PTK)
CC polypeptide subtype tyro-5. The invention provides polynucleotide
CC sequences encoding novel PTK polypeptide subtypes tyro-1 to tyro-13.
CC The PTK subtypes are found expressed predominantly in the brain tissue.
XX
SQ Sequence 57 AA:

Query Match 3.8%; Score 37; DB 19; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.4e-31;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 735 NILVNSNLVCKVSDPGLSRFLEDDTSDPTYSALGK 771
Db 1 nilvnsnlvckvsgdfglrflddtsdptysalqgk 37

RESULT 15
AAW81404
ID AAW81404 standard; Protein: 57 AA.
XX
AC AAW81404;
XX
DT 22-JAN-1999 (first entry)
XX
DE Receptor protein tyrosine kinase (PTK) subtype tyro-5.
XX
KM PTK; receptor; protein tyrosine kinase; recombinant; grafting;
KM diagnosis; tumour; skin transplant; connective tissue; tyro-5.
XX
OS Rattus sp.
XX
PM US5837448-A.
XX
PD 17-NOV-1998.
XX
PF 02-MAY-1994; 94US-0237401.
XX
PR 15-MAY-1992; 92US-0884486.
PR 02-MAY-1994; 94US-0237401.
XX
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI Lai CHC, Lemke GE;
XX
DR WPI: 1999-023436/02.
DR N-PSDB; AAV65312.
XX
PT Nucleic acids encoding protein tyrosine kinase subtypes - for
PT identification of new subtypes and treatment of diseases associated
PT with the kinase
XX
PS Claim 10: Columns 45-46; 47pp; English.
XX
CC This represents a receptor protein tyrosine kinase (PTK) subtype tyro-5.
CC The invention provides sequences AAV65308 to AAV65313, AAV65315, and
CC AAV65317 to AAV65319 that encode proteins having a tyrosine kinase domain
CC and a tissue expression pattern of a receptor PTK subtype selected from
CC tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10, tyro-11,
CC and tyro-12, respectively. The polynucleotides are useful for the
CC detection of tyrosine kinase domain sequences and detection of tissue
CC expression patterns of PTK subtypes. The cDNAs can also be injected into
CC oocytes, the protein expressed, and expression products screened for
CC using antibodies against tyrosine kinase epitopes. These subtypes
CC sequences can be used for the design of oligonucleotides, for use in
CC amplification reactions to isolate other subtype sequences. These
CC detection protocols are used in the diagnosis of diseases associated with
CC (receptor) PTKs. Recombinant vectors expressing the subtypes can be used
CC to treat related diseases e.g. tumours, by introduction of the vectors
CC into skin transplants, then grafting these into the connective tissue of
CC the dermis, thus specifically targeting tumours as the proteins are
CC released from the matrix.
XX
SQ Sequence 57 AA:

Query Match 3.8%; Score 37; DB 20; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.4e-31;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 735 NILVNSNLVCKVSDPGLSRFLEDDTSDPTYSALGK 771
Db 1 nilvnsnlvckvsgdfglrflddtsdptysalqgk 37

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